

STIC-Biotech/ChemLib

116718

From: Hamud, Fozia  
Sent: Thursday, March 11, 2004 12:54 PM  
To: STIC-Biotech/ChemLib  
Subject: search for 10/090,365

Kindly search SEQ ID NO: 48 of 10090,365 against commercial data bases and interference data bases. thanks.

Fozia Hamud  
Patent Examiner  
Art Unit 1647  
Remsen, Room 4D70  
Mail Box Remsen-4C70  
272-0884

RECEIVED  
MAR 11 2004  
STIC/Chem. Division  
(STIC)

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 3/15  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 116718**

**TO: Fozia Hamud**  
**Location: REM/4D70/4C70**  
**Art Unit: 1647**  
**Monday, March 15, 2004**  
**Case Serial Number: 10/090365**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**REM-1A65**  
**Phone: (571)272-2527**

**paul.schulwitz@uspto.gov**

### **Search Notes**

Examiner Hamud,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2527

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2004, 15:55:02 ; Search time 60 Seconds  
(without alignments)  
1083.099 Million cell updates/sec

Title: US-10-090-365-48

Perfect score: 1242

Sequence: 1 MMPKHLGLLILLSSATE.....YQPFDRSPRSKRCVHIP 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep29Jan04.\*

1: Genesep1980s.\*

2: Genesep1990s.\*

3: Genesep2000s.\*

4: Genesep2001s.\*

5: Genesep2002s.\*

6: Genesep2003as.\*

7: Genesep2003bs.\*

8: Genesep2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	230	5 AAE28616	Aae28616 Mouse Zcy
2	1234	99.4	230	5 ABJ10501	Abj10501 Cytokine
3	1224	98.6	230	5 AAE28613	Aae28613 Mouse Zcy
4	831.5	66.9	231	5 ABJ10510	Abj10510 Cytokine
5	829.5	66.8	231	5 ABJ10514	Abj10514 Cytokine
6	827.5	66.6	231	5 ABJ10519	Abj10519 Cytokine
7	826.5	66.5	231	4 AAE05048	Aae05048 Human ZCY
8	826.5	66.5	231	4 AAE28657	Aae28657 Human cyt
9	826.5	66.5	231	4 AAE02460	Aae02460 Human DNA
10	826.5	66.5	231	5 AAE28600	Aae28600 Human Zcy
11	826.5	66.5	231	5 AAE17320	Aae17320 Human cyt
12	826.5	66.5	231	5 AAO17381	Aao17381 Human cyt
13	826.5	66.5	231	5 ABJ10498	Abj10498 Cytokine
14	826.5	66.5	231	5 AEG34086	Aeg34086 Human Pro
15	826.5	66.5	231	5 AAU80000	Aau80000 Human IL-
16	826.5	66.5	231	6 AAE30826	Aae30826 Human cyt
17	826.5	66.5	231	6 AAE30838	Aae30838 Human cyt
18	826.5	66.5	231	6 ADA01382	Ada01382 Human PRO
19	826.5	66.5	231	6 ADA43811	Ada43811 Human sec
20	826.5	66.5	231	6 ADA43579	Ada43579 Human sec
21	826.5	66.5	231	6 ADA01254	Ada01254 Human PRO
22	826.5	66.5	231	7 ADA01138	Ada01138 Human sec
23	826.5	66.5	231	7 ADA43695	Ada43695 Human sec
24	826.5	66.5	231	7 ADA06957	Ada06957 Human PRO
25	826.5	66.5	231	7 ADA08445	Ada08445 Novel hum

26	826.5	66.5	231	7 ADB99738	ADB99738 Human PRO
27	826.5	66.5	231	7 ADB87021	ADB87021 Human PRO
28	826.5	66.5	231	7 ADB66176	ADB66176 Human sec
29	826.5	66.5	231	7 ADB99854	ADB99854 Human PRO
30	826.5	66.5	231	7 ADB99509	ADB99509 Novel hum
31	826.5	66.5	231	7 ADB66060	ADB66060 Human sec
32	826.5	66.5	231	7 ADC23458	ADC23458 Human tra
33	826.5	66.5	231	7 ADC26151	ADC26151 Human PRO
34	826.5	66.5	231	7 ADE04978	ADE04978 Human PRO
35	826.5	66.5	231	7 ADE11284	ADE11284 Human PRO
36	826.5	66.5	231	7 ADD88215	ADD88215 Human PRO
37	826.5	66.5	231	7 ADD95510	ADD95510 Human sec
38	826.5	66.5	231	7 ADE06440	ADE06440 Human PRO
39	826.5	66.5	231	7 ADE38215	ADE38215 Human PRO
40	826.5	66.5	231	7 ADD88331	ADD88331 Human PRO
41	826.5	66.5	231	7 ADD90912	ADD90912 Human sec
42	826.5	66.5	231	8 ADE51765	ADE51765 Human sec
43	826.5	66.5	231	8 ADE51881	ADE51881 Human sec
44	826.5	66.5	231	8 ADE37739	ADE37739 Human sec
45	826.5	66.5	231	8 ADE37623	ADE37623 Human sec

ALIGNMENTS

RESULT 1

AAE28616  
ID AAE28616 standard; protein; 230 AA.

XX AAE28616;

AC AC

DT 27-DEC-2002 (first entry)

XX

DE Mouse Zcytor16 protein #2.

XX

KW Cytokine receptor; Zcytor16; IL-TiF; autoimmune disease; dermatological;  
KW inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;  
KW asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;  
KW diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;  
KW immunosuppressive; nephrotropic; allergy; placental health; abortion;  
KW cancer; mouse.  
XX  
OS Mus musculus.

Key	Location/Qualifiers
Peptide	1..23
Protein	/label= Signal_peptide 27..230
Domain	/notes= "Mouse mature Zcytor16 protein" 31..229
Domain	/notes= "Cytokine binding domain" 31..122
Region	/note= "Fibronectin III domain I" 123..130
Domain	/note= "linker" 131..229
Domain	/note= "Fibronectin III domain II" 219..222
	/note= "Class II cytokine domain"

MO200270655-A2.

12-SEP-2002.

04-MAR-2002; 2002WO-US0006267.

02-MAR-2001; 2001US-0273035P.

27-MAR-2001; 2001US-0279232P.

(ZIMO ) ZYMOGENETICS INC.

Presnell SR, Xu W, Kindsvogel W, Chen Z;

XX

DR WPI; 2002-698750/75.  
 XX N-PSDB; AAD45989.

XX New Zcytor16 polypeptide useful for treating autoimmune or inflammatory  
 PT diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,  
 PT atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects  
 PT of IL-TIF.

XX Claim 1; Page 219-220; 221pp; English.

XX The invention relates to cytokine receptor designated as mouse Zcytor16  
 CC which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is  
 CC useful in modulating the immune system by binding Zcytor16 ligand, and  
 CC thus, preventing the binding of the ligand with endogenous Zcytor16  
 CC receptor. It is useful for studying human inflammation or immune  
 CC function, or for treating autoimmune or inflammatory diseases such as  
 CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus  
 CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,  
 CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic  
 CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-  
 CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the  
 CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene  
 CC expression and gene structure, such as in the diagnosis and/or prevention  
 CC of spontaneous abortions or in monitoring placental health and function.  
 CC It is also used in gene therapy. The present sequence is mouse Zcytor16  
 CC protein

XX Sequence 230 AA;

Query Match 100.0%; Score 1242; DB 5; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 4e-127;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSSNIIYF 60  
 DB 1 MWPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSSNIIYF 60  
 QY 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120  
 DB 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120  
 QY 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNRSQSGKASMETYYGLVYRVFTINNSLE 180  
 DB 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNRSQSGKASMETYYGLVYRVFTINNSLE 180  
 QY 181 KEQKAYEGTQRAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCVCVHIP 230  
 DB 181 KEQKAYEGTQRAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCVCVHIP 230

RESULT 2  
 ABJ10501  
 ID ABJ10501 standard; protein; 230 AA.

XX ABJ10501;

XX 21-NOV-2002 (first entry)

XX Cytokine receptor family 2 (CRF2) related protein SEQ ID No 12.

XX Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;  
 XX antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;  
 XX gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;  
 XX interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;  
 XX autoimmune disease; rheumatoid arthritis; multiple sclerosis;  
 XX inflammation.

XX Mus sp.

XX WO200266647-A2.

XX 29-AUG-2002.

XX

14-JAN-2002; 2002WO-US000986.

12-JAN-2001; 2001US-0261442P.

06-FEB-2001; 2001US-0267021P.

23-FEB-2001; 2001US-0270835P.

(GEMY ) GENETICS INST LLC.

Fouser L, Liu W, Deng B;

WPI; 2002-674946/72.

N-PSDB; ABT08221.

New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for

diagnosing and treating disorders with abnormal CRF2-12 activity such as

autoimmune diseases like rheumatoid arthritis, multiple sclerosis and

inflammation.

Claim 12; Page 13; 91pp; English.

The invention relates to an isolated type 2 cytokine receptor family  
 (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids  
 21-66 of a 231 residue amino acid sequence, given in the specification,  
 or its complement. The compositions and methods of the present invention  
 are useful for diagnosing, screening and treating disorders associated  
 with abnormal CRF2-12 activity such as autoimmune diseases like  
 rheumatoid arthritis, multiple sclerosis and inflammation. This sequence  
 represents a cytokine receptor family 2 (CRF2-12) protein relating to the  
 invention

Sequence 230 AA;

Query Match 99.4%; Score 1234; DB 5; Length 230;  
 Best Local Similarity 99.6%; Pred. No. 3e-126;  
 Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSSNIIYF 60  
 DB 1 MWPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSSNIIYF 60  
 QY 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120  
 DB 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120  
 QY 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNRSQSGKASMETYYGLVYRVFTINNSLE 180  
 DB 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNRSQSGKASMETYYGLVYRVFTINNSLE 180  
 QY 181 KEQKAYEGTQRAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCVCVHIP 230  
 DB 181 KEQKAYEGTQRAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCVCVHIP 230

RESULT 3

AAE28613

ID AAE28613 standard; protein; 230 AA.

XX AAE28613;

XX 27-DEC-2002 (first entry)

XX Mouse Zcytor16 protein #1.

XX Cytokine receptor; Zcytor16; IL-TIF; autoimmune disease; dermatological;  
 XX inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;  
 XX asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;  
 XX diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;  
 XX immunosuppressive; nephrotropic; allergy; placental health; abortion;  
 XX cancer; mouse.

OS Mus musculus.

XX Key

Location/Qualifiers

XX



Peptide 1. .23  
/label= Signal\_peptide  
Protein 24. .230  
Domain 31. .229  
Domain 31. .122  
Region 123. .130  
Domain 131. .229  
Domain 219. .222  
/note= "Class II cytokine domain"  
WO200270655-A2.  
12-SEP-2002.  
04-MAR-2002; 2002WO-US006267.  
02-MAR-2001; 2001US-0273035P.  
27-MAR-2001; 2001US-0279232P.  
(Zymo ) ZYMOGENETICS INC.  
Presnell SR, Xu W, Kindsvogel W, Chen Z;  
WPI; 2002-698750/75.  
N-PSDS; AAD45982.  
New Zcytor16 polypeptide useful for treating autoimmune or inflammatory diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma, atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects of IL-TIF.  
Claim 1; Page 213; 221pp; English.  
The invention relates to cytokine receptor designated as mouse Zcytor16 which can bind and antagonize the IL-TIF. The Zcytor16 polypeptide is useful in modulating the immune system by binding Zcytor16 ligand, and thus, preventing the binding of the ligand with endogenous Zcytor16 receptor. It is useful for studying human inflammation or immune function, or for treating autoimmune or inflammatory diseases such as inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer, diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the anti-mouse Zcytor16 antibody are useful as probes in detecting gene expression and gene structure, such as in the diagnosis and/or prevention of spontaneous abortions or in monitoring placental health and function. It is also used in gene therapy. The present sequence is mouse Zcytor16 protein  
Sequence 230 AA;  
Query Match 98.6%; Score 1224; DB 5; Length 230;  
Best Local Similarity 99.1%; Pred. No. 3.7e-125; Indels 0; Gaps 0;  
Matches 228; Conservative 0; Mismatches 2;  
QY 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIYF 60  
DB 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIYF 60  
QY 61 VOYKXGQSQHEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRTRPF 120  
DB 61 VOYKXGQSQHEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRTRPF 120  
QY 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPRNQSGKNASMETYYGLVYRVFTINNSL 180  
DB 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPRNQSGKNASMETYYGLVYRVFTINNSL 180

QY 181 KEQKAYEGTORAVEIEGLIPHSYCVVAEMTQPMFDRSPRSKRCVHIP 230  
DB 181 KEQKAYEGTORAVEIEGLIPHSYCVVAEMTQPMFDRSPRSKRCVQIP 230  
RESULT 4  
ID ABJ10510 standard; protein; 231 AA.  
XX ABJ10510;  
XX 21-NOV-2002 (first entry)  
XX Cytokine receptor family 2 (CRF2) related protein SEQ ID No 21.  
XX Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;  
XX antinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;  
XX gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;  
XX interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;  
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis;  
XX inflammation.  
XX Unidentified.  
XX WO200266647-A2.  
XX 29-AUG-2002.  
XX 14-JAN-2002; 2002WO-US000986.  
XX 12-JAN-2001; 2001US-0261442P.  
XX 06-FEB-2001; 2001US-0267021P.  
XX 23-FEB-2001; 2001US-0270835P.  
XX (GEMV ) GENETICS INST LLC.  
XX Fouser L, Liu W, Deng B;  
XX WPI; 2002-674946/72.  
XX New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for  
XX diagnosing and treating disorders with abnormal CRF2-12 activity such as  
XX autoimmune diseases like rheumatoid arthritis, multiple sclerosis and  
XX inflammation.  
XX Example 11; Page 78; 91pp; English.  
XX The invention relates to an isolated type 2 cytokine receptor family  
XX (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids  
XX 21-66 of a 231 residue amino acid sequence, given in the specification,  
XX or its complement. The compositions and methods of the present invention  
XX are useful for diagnosing, screening and treating disorders associated  
XX with abnormal CRF2-12 activity such as autoimmune diseases like  
XX rheumatoid arthritis, multiple sclerosis and inflammation. This sequence  
XX represents a cytokine receptor family 2 (CRF2-12) protein relating to the  
XX invention  
XX Sequence 231 AA;  
Query Match 66.9%; Score 831.5; DB 5; Length 231;  
Best Local Similarity 67.1%; Pred. No. 3.4e-82;  
Matches 155; Conservative 20; Mismatches 55; Indels 1; Gaps 1;  
QY 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 59  
DB 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 60  
QY 60 VOYKXGQSQHEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRTRPF 119  
DB 61 VOYKXGQSQHEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRTRPF 120  
QY 120 PWWETKLDPPVVTITRVNASLRVLLRPPELPRNQSGKNASMETYYGLVYRVFTINNSL 179

```
Db 121 TPWWTETKIDPPVNMITQVNGSLVILHAPNLPYRYQKKNVSIEDYYELLYRVFIINNSL 180
QY 180 EKEQKAYECTQRAVEIEGLIPHSSYCVVAEMYPQWFDPRSRSKERCVCCHIP 230
Db 181 EKEQKVEGAHRAVEIEALTPHSSYCVVAETIYQPMIDRRSQSERCVCVEIP 231

RESULT 5
ID ABJ10514
XX ABJ10514 standard; protein; 231 AA.
AC ABJ10514;
XX
DT 21-NOV-2002 (first entry)
XX
DE Cytokine receptor family 2 (CRF2) related protein SEQ ID No 25.
XX
KW Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW inflammation.
XX
OS Unidentified.
XX
PN WO200266647-A2.
XX
PD 29-AUG-2002.
XX
PF 14-JAN-2002; 2002WO-US000986.
XX
PR 12-JAN-2001; 2001US-0261442P.
XX
PR 06-FEB-2001; 2001US-0267021P.
XX
PR 23-FEB-2001; 2001US-0270835P.
XX
PA (GEMY ) GENETICS INST LLC.
XX
PI Fouser L, Liu W, Deng B;
XX
PI WPI; 2002-674946/72.
XX
DR
XX
PT New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
PT diagnosing and treating disorders with abnormal CRF2-12 activity such as
PT autoimmune diseases like rheumatoid arthritis, multiple sclerosis and
PT inflammation.
XX
PS Example 15; Page 79; 91pp; English.
XX
CC The invention relates to an isolated type 2 cytokine receptor family
CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
CC 21-66 of a 231 residue amino acid sequence, given in the specification,
CC or its complement. The compositions and methods of the present invention
CC are useful for diagnosing, screening and treating disorders associated
CC with abnormal CRF2-12 activity such as autoimmune diseases like
CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
CC invention
XX
SQ Sequence 231 AA;
Query Match 66.8%; Score 829.5; DB 5; Length 231;
Best Local Similarity 67.1%; Pred. No. 5.6e-82;
Matches 155; Conservative 19; Mismatches 56; Indels 1; Gaps 1;
QY 1 MNPKHCLGLLI-ILSSATEIQARVSLTPQKRVQSRNFHNLHWQAGSLPNSNIY 59
Db 1 MNPKHCFGLGFLISFFLTGVAGTQSTHESLKPQKRVQSRNFHNLQWQGRALTGNSVY 60
QY 60 FVQYKXGQSQWEDKVDGCTTALFCDLTNETLDPVELYVGYGWTACAGHSAWTTBPF 119
Db 61 FVQYKYGQKWKEDCWGCTQLSCLTSETSDIOETPIYGRVRAASAGSISEWNTBPF 120
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QY 120 TPWWTETKIDPPVNMITRVNASLRVLLRPPELPRNRQSGKQASMETTYGIVYRVFTINNSL 179
Db 121 TPWWTETKIDPPVNMITQVNGSLVILHAPNLPYRYQKKNVSIEDYYELLYRVFIINNSL 180
QY 180 EKEQKAYECTQRAVEIEGLIPHSSYCVVAEMYPQWFDPRSRSKERCVCCHIP 230
Db 181 EKEQKVEGAHRAVEIEALTPHSSYCVVAETIYQPMIDRRSQSERCVCVEIP 231

RESULT 6
ID ABJ10519
XX ABJ10519 standard; protein; 231 AA.
AC ABJ10519;
XX
DT 21-NOV-2002 (first entry)
XX
DE Cytokine receptor family 2 (CRF2) related protein SEQ ID No 30.
XX
KW Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW inflammation.
XX
OS Unidentified.
XX
PN WO200266647-A2.
XX
PD 29-AUG-2002.
XX
PF 14-JAN-2002; 2002WO-US000986.
XX
PR 12-JAN-2001; 2001US-0261442P.
XX
PR 06-FEB-2001; 2001US-0267021P.
XX
PR 23-FEB-2001; 2001US-0270835P.
XX
PA (GEMY ) GENETICS INST LLC.
XX
PI Fouser L, Liu W, Deng B;
XX
PI WPI; 2002-674946/72.
XX
DR
XX
PT New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
PT diagnosing and treating disorders with abnormal CRF2-12 activity such as
PT autoimmune diseases like rheumatoid arthritis, multiple sclerosis and
PT inflammation.
XX
PS Example 20; Page 81; 91pp; English.
XX
CC The invention relates to an isolated type 2 cytokine receptor family
CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
CC 21-66 of a 231 residue amino acid sequence, given in the specification,
CC or its complement. The compositions and methods of the present invention
CC are useful for diagnosing, screening and treating disorders associated
CC with abnormal CRF2-12 activity such as autoimmune diseases like
CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
CC invention
XX
SQ Sequence 231 AA;
Query Match 66.8%; Score 827.5; DB 5; Length 231;
Best Local Similarity 67.1%; Pred. No. 9.2e-82;
Matches 155; Conservative 19; Mismatches 56; Indels 1; Gaps 1;
QY 1 MNPKHCLGLLI-ILSSATEIQARVSLTPQKRVQSRNFHNLHWQAGSLPNSNIY 59
Db 1 MNPKHCFGLGFLISFFLTGVAGTQSTHESLKPQKRVQSRNFHNLQWQGRALTGNSVY 60
QY 60 FVQYKXGQSQWEDKVDGCTTALFCDLTNETLDPVELYVGYGWTACAGHSAWTTBPF 119
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Db 61 FVOYKIYQORQWKNKDCWGTQELSCDLTSETSDIQEPYIGRVRAAGSAGSYSEWSMTRF 120  
QY 120 TPWETKLDPPVVTITRVNASLVLRLPPELPNRSQSGKASMETYYGLVYRVFTINNSL 179  
Db 121 TPWETKIDPPVPMNITQVNGSLVLILHAPNLPYRYQKEKNVSIEDYVELLYRVFTINNSL 180  
QY 180 EKEQKAYEGTQRAVEIEGLIPHSSYCVVAEMYPQMFDRSPRSKERCVCVHIP 230  
Db 181 EKEQKAYEGAHRAVEIEALTTHSSYCVVAEIYQPMIDRRSQSRSERCVEIP 231  
RESULT 7  
AAE05048  
ID AAE05048 standard; protein; 231 AA.  
XX  
AC AAE05048;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human ZCYTO18 soluble receptor antagonist, zcytor16 protein.  
XX  
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;  
XX cancer; inflammation; gene therapy; zcytor16.  
OS Homo sapiens.  
XX  
PN WO200146422-A1.  
XX  
PD 28-JUN-2001.  
XX  
PF 22-DEC-2000; 2000WO-US035308.  
XX  
PR 23-DEC-1999; 99US-00471767.  
PR 01-DEC-2000; 2000US-0250841P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Presnell SR, Kindsvogel W;  
XX  
XX WPI: 2001-408648/43.  
DR N-PSDB; AAD09745.  
XX  
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.  
XX  
PS Example 13A; Page 158-159; 167pp; English.  
XX  
CC The patent discloses novel human cytokine, ZCYTO18 protein and its  
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells  
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in  
CC K562 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in  
CC a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer  
CC and inflammation. ZCYTO18 protein is useful for killing cancer cells. It  
CC is useful for increasing platelets in a patient or injured tissue. It is  
CC also used in gene therapy. The present sequence is human zcytor16, which  
CC is a naturally expressed soluble receptor antagonist of ZCYTO18 protein  
XX  
SQ Sequence 231 AA;  
Query Match 66.5%; Score 826.5; DB 4; Length 231;  
Best Local Similarity 66.7%; Pred No. 1.2e-81;  
Matches 134; Conservative 20; Mismatches 56; Indels 1; Gaps 1;  
QY 1 MNPKHCLGLLI-ILSSATEIQPARVSTPQKVFQSRNFNHLHWAGSLPNNIY 59  
Db 1 MNPKHCLGLISFLTGVAGTQSTHESLKQVRQFSRNFNHLQWQPGRLTGNSSV 60  
QY 60 FVOYKMGYQOSQWEDKVDGWTALFCDLTNETLDPVELYIGRVMTACGRHSMTTRPF 119  
Db 61 FVOYKIYQORQWKNKDCWGTQELSCDLTSETSDIQEPYIGRVRAAGSAGSYSEWSMTRF 120  
QY 120 TPWETKLDPPVVTITRVNASLVLRLPPELPNRSQSGKASMETYYGLVYRVFTINNSL 179  
Db 121 TPWETKIDPPVPMNITQVNGSLVLILHAPNLPYRYQKEKNVSIEDYVELLYRVFTINNSL 180

QY 180 EKEQKAYEGTQRAVEIEGLIPHSSYCVVAEMYPQMFDRSPRSKERCVCVHIP 230  
Db 181 EKEQKAYEGAHRAVEIEALTTHSSYCVVAEIYQPMIDRRSQSRSERCVEIP 231  
RESULT 8  
AAB62657  
ID AAB62657 standard; protein; 231 AA.  
XX  
AC AAB62657;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Human cytokine receptor, zcytor16.  
XX  
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;  
XX antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;  
XX immunosuppressive; chromosome 9q24.1-25.2; human.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT Domain 22..231  
FT /note= "extracellular domain"  
FT Domain 22..108  
FT /note= "Ig domain 1"  
FT Domain 112..210  
FT /note= "Ig domain 2"  
XX  
PN WO200140467-A1.  
XX  
PD 07-JUN-2001.  
XX  
PF 01-DEC-2000; 2000WO-US032703.  
XX  
PR 03-DEC-1999; 99US-0169049P.  
PR 13-SEP-2000; 2000US-0232219P.  
PR 31-OCT-2000; 2000US-0244610P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Presnell SR, Xu W, Kindsvogel W, Chen Z;  
XX  
XX WPI: 2001-356158/37.  
DR N-PSDB; AAF83735.  
XX  
XX New soluble cytokine receptor polypeptides and polynucleotides, useful  
XX for diagnosing and treating cancer and inflammatory conditions.  
XX  
XX Claim 1; Page 186-188; 210pp; English.  
XX  
XX The invention relates to a human cytokine receptor polypeptide,  
XX designated zcytor16. The zcytor16 polypeptide can be expressed by  
XX standard recombinant methodology and can bind to IL-TIF (undefined). The  
XX zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation  
XX or differentiation of hematopoietic cell(s) (progenitors); reducing IL-  
XX TIF induced or IL-9 induced inflammation; and suppressing an inflammatory  
XX response in a mammal with inflammation. Heteromeric/ multimeric receptor  
XX polypeptides such as soluble zcytor 16/CRP2-4 can be used to reduce  
XX progression and symptoms of cancer. Zcytor16 polypeptides can also be  
XX used to detect IL-TIF levels which is indicative of pathological  
XX conditions including inflammatory states (e.g. rheumatoid arthritis) and  
XX cancer. Antibodies that bind zcytor16 polypeptides and the polypeptides  
XX themselves are useful for the treatment of inflammation, inflammatory  
XX diseases (e.g. infection, asthma, inflammatory bowel disease, rheumatoid  
XX arthritis and atherosclerosis) and autoimmune diseases. The antibodies  
XX and zcytor16 polynucleotides are also useful for detecting cancer. The  
XX present sequence represents the human zcytor16 protein  
XX  
SQ Sequence 231 AA;  
Query Match 66.5%; Score 826.5; DB 4; Length 231;

Best Local Similarity 66.7%; Pred. No. 1.2e-81;  
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;

QY 1 MPPKHCILGLLI-ILSSATEIQPARVSLTPQKVFQSRNFHNLHWAGSLPSNNSIY 59  
DB 1 MPPKHCFLGLISFFLTGVAGTQSTHESLKPVQFQSRNFHNLHWAGSLPSNNSIY 60  
QY 60 FVQYKMYGQSWEDKVDWGTTFALFCDLTNETLDPYELVYGRVMTACAGHSATRTPRF 119  
DB 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPPYGRVRAASAGSYSEWSMTPRF 120  
QY 120 TPWETKLDPPVVTITRVNASLRLVLRPPPELNRNOSGKNASMETYYGLVYRVFTINNSL 179  
DB 121 TPWETKIDPPVNNITQVNGSLVLHAPNLVRYQKEKVSIEDYVELLYRVFIINNSL 180  
QY 180 EKEQKAYEGTORAVEIEGLIPHSYCVVAEMYPMPDRSPRSKRCVHIP 230  
DB 181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQRSERCVEIP 231

RESULT 9  
AAE02460  
ID AAE02460 standard; protein; 231 AA.  
AC AAE02460;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human DNAX cytokine receptor subunit 4.2 (DCRS4.2).  
XX  
KW Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;  
KW therapy; immunological disorder; drug screening; cell development;  
KW chromosome 6q24.1-25.2.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT Protein 22..231  
FT /label= DCRS4.2  
FT /note= "Human mature DNAX cytokine receptor subunit 4.2"  
XX  
PN W0200136467-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 16-NOV-2000; 2000WO-US031363.  
XX  
PR 18-NOV-1999; 99US-00443060.  
XX  
PR 13-DEC-1999; 99US-0170320P.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM;  
XX  
DR WPI; 2001-343800/36.  
DR N-PSDB; AAD06414.  
XX  
FT New mammalian receptor proteins related to cytokine receptors, useful for  
FT regulating cell development and for diagnosis and treatment of  
FT immunological disorders.  
XX  
PS Claim 3; Page 23; 124pp; English.  
XX  
CC The present sequence is human DNAX cytokine receptor subunit 4.2  
CC (DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2. Cytokine  
CC receptors, fragments and antibodies are useful for treating immunological  
CC disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are useful in drug  
CC screening to identify compounds having binding affinity to the receptor  
CC subunit. Modulators of DCRS are useful for modulating the physiology or  
CC development of a cell or tissue culture cells. A purified DCRS is useful  
CC as a reagent to detect antibodies generated in response to the presence

of elevated levels of expression, or immunological disorders which lead  
to production of antibody to the endogenous receptor. Cytokine receptor  
sequences are useful as probes for detecting levels of the cytokine  
receptor in patients suspected of having an immunological disorder.  
Antibodies have therapeutic value, are useful as potent antagonist, in  
detecting or quantifying ligands, for isolating DCRS proteins and  
peptides, to screen expression libraries for particular expression  
products, to raise anti-idiotypic antibodies and for detecting or  
diagnosing various immunological conditions related to expression of the  
protein or cells which express the protein

QY Sequence 231 AA;  
Query Match 66.5%; Score 826.5; DB 4; Length 231;  
Best Local Similarity 66.7%; Pred. No. 1.2e-81;  
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;

QY 1 MPPKHCILGLLI-ILSSATEIQPARVSLTPQKVFQSRNFHNLHWAGSLPSNNSIY 59  
DB 1 MPPKHCFLGLISFFLTGVAGTQSTHESLKPVQFQSRNFHNLHWAGSLPSNNSIY 60  
QY 60 FVQYKMYGQSWEDKVDWGTTFALFCDLTNETLDPYELVYGRVMTACAGHSATRTPRF 119  
DB 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPPYGRVRAASAGSYSEWSMTPRF 120  
QY 120 TPWETKLDPPVVTITRVNASLRLVLRPPPELNRNOSGKNASMETYYGLVYRVFTINNSL 179  
DB 121 TPWETKIDPPVNNITQVNGSLVLHAPNLVRYQKEKVSIEDYVELLYRVFIINNSL 180  
QY 180 EKEQKAYEGTORAVEIEGLIPHSYCVVAEMYPMPDRSPRSKRCVHIP 230  
DB 181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQRSERCVEIP 231

RESULT 10  
AAE28600  
ID AAE28600 standard; protein; 231 AA.  
AC AAE28600;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human Zcytor16 protein.  
XX  
KW Cytokine receptor; Zcytor16; IL-TIF; autoimmune disease; dermatological;  
KW inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;  
KW asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;  
KW diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;  
KW immunosuppressive; nephrotropic; allergy; placental health; abortion;  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT Protein 23..231  
FT /label= Signal\_peptide  
FT /note= "Mouse mature Zcytor16 protein"  
FT Domain 32..230  
FT /note= "Cytokine binding domain"  
FT Domain 32..123  
FT /note= "Fibronectin III domain I"  
FT Region 124..131  
FT /note= "Linker"  
FT Domain 132..230  
FT /note= "Fibronectin III domain II"  
FT Domain 220..223  
FT /note= "Class II cytokine domain"  
XX  
PN W0200270655-A2.  
XX  
PD 12-SEP-2002.  
XX

PF 04-MAR-2002; 2002WO-US006267.  
XX  
PR 02-MAR-2001; 2001US-0273035P.  
PR 27-MAR-2001; 2001US-0279232P.  
XX  
PA (ZYMO) ZYMOGENETICS INC.  
XX  
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;  
XX  
DR WPI; 2002-698750/75.  
DR N-PSDB; AAD45959.  
XX  
XX New Zcytor16 polypeptide useful for treating autoimmune or inflammatory  
PT diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,  
PT atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects  
PT of IL-TIF.  
XX  
PS Example 1; Page 191; 221pp; English.  
XX  
CC The invention relates to cytokine receptor designated as mouse Zcytor16  
CC which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is  
CC useful in modulating the immune system by binding Zcytor16 ligand, and  
CC thus, preventing the binding of the ligand with endogenous Zcytor16  
CC receptor. It is useful for studying human inflammation or immune  
CC function, or for treating autoimmune or inflammatory diseases such as  
CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus  
CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,  
CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic  
CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-  
CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the  
CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene  
CC expression and gene structure, such as in the diagnosis and/or prevention  
CC of spontaneous abortions or in monitoring placental health and function.  
CC It is also used in gene therapy. The present sequence is human Zcytor16  
CC protein. Human Zcytor16 gene resides at chromosome 6  
XX  
XX Sequence 231 AA;  
XX  
Query Match 66.5%; Score 826.5; DB 5; Length 231;  
Best Local Similarity 66.7%; Pred. No. 1.2e-81;  
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;  
QY 1 MNPKECLGLI-ILLSSATEIPARVSLTPKQRFQSRNFHNLHWAGSLPNSNIY 59  
DB 1 MNPKECFGLFLISFLTVAGTQSTHESLKQRFQSRNFHNLHWQPGRLTGNISVY 60  
QY 60 FVQYKMGOSQWEDKVDGWTGTTALPCDLTNETLDPYELLYGRVMTACGRHSAMTRPRF 119  
DB 61 FVQYKIYQORQWKNEDCWGTQELSCDLTSETSDIQEYKGRVRAASAGSYSEWSMTPRF 120  
QY 120 TPWETKIDPPVVTITRVNASLRLRPELPENRQSGKNSMETYYGLVYRFTINNSL 179  
DB 121 TPWETKIDPPVNMNITQVNGSLVILHAPNUPYRYQKERNVSIEDYELLRYRFTINNSL 180  
QY 180 EKEQKAYGTORAVIEGLIPHSYCVVAEMYPQMFDRSRKRCVHP 230  
DB 181 EKEQKVGAGRAVIEALTPHSYCVVAELIYQPMIDRRSQRSEBRCVEIP 231  
RESULT 11  
AAE17320  
ID AAE17320 standard; protein; 231 AA.  
XX  
AC AAE17320;  
XX  
XX 18-APR-2002 (first entry)  
DT  
XX Human cytokine receptor protein, sbg456548CytoRa #2.  
DE  
XX Human; therapy; wound healing disorder; vaccine; cancer; infection;  
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;  
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;  
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;  
KW

KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;  
KW depression; cardiovascular disease; myocardial infarction; renal failure;  
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen failure;  
KW type II diabetes mellitus; skeletal muscle disease; immunosuppressive;  
KW hyperplasia; renal disease; hypoglycaemia; gastrointestinal disease;  
KW neutropenia; Hodgkin's disease; neuroleptic; anti-inflammatory;  
KW haemostatic; vulvovaginitis; anticonvulsant; antirheumatic; neuroprotective;  
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebrotropic;  
KW allergy; cytokine receptor.  
XX  
OS Homo sapiens.  
XX  
XX WO200198342-A1.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US019929.  
XX  
XX 22-JUN-2000; 2000US-0213156P.  
PR 22-JUN-2000; 2000US-0213161P.  
XX  
XX (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (GLAX) GLAXO GROUP LTD.  
XX  
XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SH;  
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;  
XX  
XX WPI; 2002-139783/18.  
DR N-PSDB; AAD27815.  
XX  
XX Novel secreted and membrane-associated polypeptides and polynucleotides  
PT useful for preventing, ameliorating or correcting dysfunction or disease  
PT including diabetes, cancer, hypertension and growth abnormalities.  
XX  
XX Claim 1; Page 132-133; 138pp; English.  
XX  
CC The invention relates to secreted and membrane-associated polypeptides  
CC and polynucleotides. The sequences of the invention are useful in  
CC diagnostic assays for detecting diseases associated with inappropriate  
CC activity or levels of these polynucleotides, and in identifying their  
CC agonists and antagonists that are potentially useful in therapy. The  
CC sequences of the invention are useful as vaccines for inducing  
CC immunological response. The sequences of the invention are useful for  
CC treating cancers, infections, autoimmune disorders, haematopoietic  
CC disorders, wound healing disorders, cholesterol ester storage disease,  
CC inflammation, congenital muscular dystrophy, functional epidermolysis  
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,  
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,  
CC allergies, schizophrenia, sbg44245PROA-associated disorders,  
CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,  
CC graft versus host disease, ischaemia, stroke, acute respiratory disease  
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,  
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,  
CC depression, anxiety disorders and sleep disorders, cardiovascular  
CC diseases including congestive heart failure and myocardial infarction,  
CC respiratory diseases including chronic obstructive pulmonary disease,  
CC acute bronchitis and adult respiratory distress syndrome, liver disorders  
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral  
CC and non-viral hepatitis, type II diabetes mellitus, renal disease  
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's  
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
CC and tendinitis, gastrointestinal diseases including intestinal  
CC obstruction and tropical sprue, spleen disorders including hypersplenism,  
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male  
CC reproductive diseases including low testosterone and male infertility.  
CC The present sequence is human cytokine receptor  
XX  
XX Sequence 231 AA;  
XX  
Query Match 66.5%; Score 826.5; DB 5; Length 231;  
Best Local Similarity 66.7%; Pred. No. 1.2e-81;  
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;  
QY 1 MNPKECLGLI-ILLSSATEIPARVSLTPKQRFQSRNFHNLHWAGSLPNSNIY 59  
DB 1 MNPKECFGLFLISFLTVAGTQSTHESLKQRFQSRNFHNLHWQPGRLTGNISVY 60  
QY 60 FVQYKMGOSQWEDKVDGWTGTTALPCDLTNETLDPYELLYGRVMTACGRHSAMTRPRF 119  
DB 61 FVQYKIYQORQWKNEDCWGTQELSCDLTSETSDIQEYKGRVRAASAGSYSEWSMTPRF 120  
QY 120 TPWETKIDPPVVTITRVNASLRLRPELPENRQSGKNSMETYYGLVYRFTINNSL 179  
DB 121 TPWETKIDPPVNMNITQVNGSLVILHAPNUPYRYQKERNVSIEDYELLRYRFTINNSL 180  
QY 180 EKEQKAYGTORAVIEGLIPHSYCVVAEMYPQMFDRSRKRCVHP 230  
DB 181 EKEQKVGAGRAVIEALTPHSYCVVAELIYQPMIDRRSQRSEBRCVEIP 231  
RESULT 11  
AAE17320  
ID AAE17320 standard; protein; 231 AA.  
XX  
AC AAE17320;  
XX  
XX 18-APR-2002 (first entry)  
DT  
XX Human cytokine receptor protein, sbg456548CytoRa #2.  
DE  
XX Human; therapy; wound healing disorder; vaccine; cancer; infection;  
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;  
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;  
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;  
KW



Query Match 66.5%; Score 826.5; DB 5; Length 231;  
Best Local Similarity 66.7%; Pred. No. 1.2e-81;  
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;  
QY 1 MWPKECHLLGLLI-LLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 59  
DB 1 MWPKECHFLGLISFLTGAGTQSTHESLXKQRFQSRNFHNLQWPGALTGNSVY 60  
QY 60 FVOYKMGQSQWEDKVCWGTGTTALFCDLTNETLDPYELLYGRVMTACAGRHSAWTRPRF 119  
DB 61 FVOYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPFYGRVRAASAGSYSEWSMTPRF 120  
QY 120 TPWETKLDPPVVTITRVNASLRVLLRPPELNNRQSGKNASMETYYGLVYRVFTINNSL 179  
DB 121 TPWETKIDPPVMTITQVNGSLLVILHAFNLPYRYQKEKNSIEDYELLYRVFTINNSL 180  
QY 180 EKEQKAYEGTQRAVEIEGLPHSSYCVVAEMYPQMFDRRSPRSCVHIP 230  
DB 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAETIQPMLDRRSQREERCVEIP 231

RESULT 14  
ABG34086  
ID ABG34086 standard; protein; 231 AA.  
AC ABG34086;  
XX  
XX 15-JUL-2002 (first entry)  
XX Human Pro peptide #57.  
XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;  
XX tumour; cancer.  
XX Homo sapiens.  
XX WO200224858-A2.  
XX 28-MAR-2002.  
XX 29-AUG-2001; 2001WO-US027099.  
XX 01-SEP-2000; 2000US-0229896P.  
XX 05-SEP-2000; 2000US-0230621P.  
XX 22-SEP-2000; 2000US-0235147P.  
XX 10-NOV-2000; 2000WO-US030873.  
XX 12-JAN-2001; 2001US-0261878P.  
XX 16-JAN-2001; 2001US-0261910P.  
XX 16-JAN-2001; 2001US-0261939P.  
XX 16-JAN-2001; 2001US-0262150P.  
XX 25-JAN-2001; 2001US-0264395P.  
XX 02-FEB-2001; 2001US-0266421P.  
XX 09-FEB-2001; 2001US-0267623P.  
XX 28-FEB-2001; 2001WO-US006520.  
XX 09-MAR-2001; 2001US-0274399P.  
XX 03-APR-2001; 2001US-0280982P.  
XX 04-APR-2001; 2001US-0282129P.  
XX 09-MAY-2001; 2001US-0290589P.  
XX 25-MAY-2001; 2001WO-US017092.  
XX 01-JUN-2001; 2001WO-US017800.  
XX 20-JUN-2001; 2001WO-US019692.  
XX 29-JUN-2001; 2001WO-US021066.  
XX 09-JUL-2001; 2001WO-US021735.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
XX Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
XX Fong S;  
XX WPI; 2002-362426/39.

DR N-PSDB; ABK70017.  
XX New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or for  
PT genetic analysis of individuals with genetic disorders.  
XX Claim 11; Fig 114; 218pp; English.  
XX This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The invention  
CC also comprises a method for producing the proteins of the invention by  
CC recombinant means and antibodies specific for the protein of the  
CC invention. The antibody may be used for detecting the PRO proteins of the  
CC invention and may be used to modify their activity. polynucleotides may  
CC be used as hybridisation probes for a cDNA library to isolate the full-  
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation  
CC probes for mapping the gene which encodes that PRO and for genetic  
CC analysis of individuals with genetic disorders, in assays to identify  
CC other proteins or molecules involved in binding reaction, to generate  
CC transgenic animals or knock-out animals which in turn are useful in the  
CC development and screening of therapeutically useful reagents, for  
CC chromosome identification, and tissue typing. The PRO polypeptides are  
CC useful in gene therapy, and as molecular weight markers for protein  
CC electrophoresis purposes. The sequences may also be used to detect  
CC overexpression on PRO polypeptides in cancerous tumours and for screening  
CC for differentially expressed genes using microarray technology. The  
CC present sequence represents a human PRO protein of the invention  
XX  
XX Sequence 231 AA;  
SQ

Query Match 66.5%; Score 826.5; DB 5; Length 231;  
Best Local Similarity 66.7%; Pred. No. 1.2e-81;  
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;  
QY 1 MWPKECHLLGLLI-LLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 59  
DB 1 MWPKECHFLGLISFLTGAGTQSTHESLXKQRFQSRNFHNLQWPGALTGNSVY 60  
QY 60 FVOYKMGQSQWEDKVCWGTGTTALFCDLTNETLDPYELLYGRVMTACAGRHSAWTRPRF 119  
DB 61 FVOYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPFYGRVRAASAGSYSEWSMTPRF 120  
QY 120 TPWETKLDPPVVTITRVNASLRVLLRPPELNNRQSGKNASMETYYGLVYRVFTINNSL 179  
DB 121 TPWETKIDPPVMTITQVNGSLLVILHAFNLPYRYQKEKNSIEDYELLYRVFTINNSL 180  
QY 180 EKEQKAYEGTQRAVEIEGLPHSSYCVVAEMYPQMFDRRSPRSCVHIP 230  
DB 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAETIQPMLDRRSQREERCVEIP 231

RESULT 15  
AAU80000  
ID AAU80000 standard; protein; 231 AA.  
XX  
XX AAU80000;  
XX  
XX 15-JUL-2002 (first entry)  
XX Human IL-TIF/IL-22 binding protein #1.  
XX Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;  
XX IL-TIF/IL-22 antagonist.  
XX Homo sapiens.  
XX WO200224912-A2.  
XX 28-MAR-2002.  
XX 21-SEP-2001; 2001WO-US029576.  
XX 22-SEP-2000; 2000US-0234583P.

PR 03-NOV-2000; 2000US-0245495P.  
PR 31-JUL-2001; 2001US-00919162.  
XX (LUDW-) LUDWIG INST CANCER RES.  
FA  
XX  
XX Renauld J, Dumoutier L;  
XX  
XX WPI; 2002-383190/41.  
DR N-PSDB; ABK50076.  
XX  
XX Polynucleotide and polypeptide of soluble protein which binds to  
PT interleukin-Tif/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a  
PT cell.  
XX  
XX  
PS Claim 14; Page 39; 42pp; English.  
XX  
XX The present invention relates to a new polynucleotide that encodes a  
CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred  
CC to as IL-22BP), where the complementary sequence of the invention  
CC hybridises under stringent conditions to a nucleotide sequence of 2271 or  
CC 2366 base pairs, as given in the specification. The molecules of the  
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22  
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,  
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably  
CC in vitro, and for obtaining an antibody molecule specific for the soluble  
CC binding protein of the invention, from a population or panel of antibody  
CC molecules of diverse binding specificity. The soluble protein is further  
CC useful in manufacture of a medicament for treating an IL-22 mediated  
CC disease and for assaying an agent, preferably an antibody or a peptide  
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding  
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is  
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated  
CC disorder. The antibody is useful for determining presence of the soluble  
CC protein, where the antibody is detectably labelled. The present amino  
CC acid sequence represents the human IL-TIF/IL-22 binding protein #1 of the  
XX invention  
XX  
SQ Sequence 231 AA;  
Query Match 56.5%; Score 826.5; DB 5; Length 231;  
Best Local Similarity 66.7%; Pred. No. 1.2e-81;  
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;  
Qy 1 MPPKHCILGLLI-ILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSY 59  
Db 1 MPPKHCFLGLISFFLTGVAGTQSTHESLKPQVQFSRNFHNLQWPGRALTGNSVY 60  
Qy 60 FVQYKMYQSQWEDKVCWGTTFALFCDLTNETLDPVELYGYRYMTACAGHSAWTRTF 119  
Db 61 FVQYKIYQKQWKNKEDCWGTQELSCDLSQTSQDIQEPYIGRVRAASAGSISWSTPR 120  
Qy 120 TPWNETKLDPPVVTITRVNASRLVLLRPPELPNRNQSGKNASMETYYGLVYRVFTINSL 179  
Db 121 TPWNETKIDPPVNNITQVNGSLVILHAPNLPYRYQKKNVSIEDYYELLYRVFIINSL 180  
Qy 180 EKEQKAYEKTORAVEIEGLIPHSYCVVAEMYQDMPDRSRPSKRCVHP 230  
Db 181 EKEQKVEGAHRAVEIEALTPHSYCVVAETIQPMLDRSRSEERCVEIP 231

Search completed: March 12, 2004, 15:58:07  
Job time : 62 secs



GenCore version 5.1.6  
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DM protein - protein search, using sw model  
Run on: March 12, 2004, 15:56:57 ; Search time 20 Seconds  
(without alignments)  
1106.203 Million cell updates/sec

Title: US-10-090-365-48  
Perfect score: 1242  
Sequence: 1 MPKHCILGLLIILSSATE.....YQPMFDRSPRSKRCVHIP 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: Pirl1.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	174.5	14.0	575	2 A49667	interleukin-10 rec
2	174.5	14.0	578	2 I56215	interleukin-10 rec
3	173	13.9	349	2 JC6311	interferon recepto
4	165.5	13.3	489	2 A31555	interferon gamma r
5	153	12.3	325	2 A47003	cytokine receptor
6	150	12.1	292	1 KFB03	tissue factor prec
7	145.5	11.7	295	1 KFB03	tissue factor prec
8	144.5	11.6	292	1 KFB3	interferon alpha/b
9	140	11.3	590	2 A45283	tissue factor prec
10	138.5	11.2	294	1 KFM53	tissue factor prec
11	138.5	11.2	477	2 A34368	interferon gamma r
12	134.5	10.8	560	2 S27387	interferon alpha r
13	123.5	9.9	331	2 A54295	interferon alpha/b
14	123.5	9.9	331	2 S59501	interferon recepto
15	122.5	9.9	515	2 I39073	interferon alpha-b
16	120.5	9.7	557	2 A32694	interferon alpha/b
17	110	8.9	337	2 I38500	interferon gamma r
18	99	8.0	2029	1 TDFLX	protein-tyrosine-p
19	95.5	7.7	332	2 A49947	interferon gamma r
20	93	7.5	272	2 JQ1802	B8R 31K protein pr
21	93	7.5	1607	2 T43212	insulin-like growt
22	92	7.4	266	2 I36855	gene B9R protein -
23	92	7.4	272	2 G42526	B8R protein - vacc
24	91.5	7.4	379	2 T19773	hypothetical prote
25	90	7.2	266	2 T28607	hypothetical prote
26	90	7.2	266	2 T28172	H9R protein - vari
27	87.5	7.0	562	2 C72278	hypothetical prote
28	85.5	6.9	202	2 H69495	conserved hypothet
29	85.5	6.9	263	2 A44229	interferon-gamma r

30	84.5	6.8	1443	2 I50600	neogenin - chicken
31	81.5	6.6	674	2 A47222	Kallmann syndrome
32	81.5	6.6	676	2 B47222	Kallmann syndrome
33	81.5	6.6	792	2 SI6680	ribonucleoside-dip
34	81.5	6.6	1209	2 T42718	probable neural ce
35	81.5	6.6	1608	1 WMTGM	interleukin-3 rece
36	81	6.5	896	2 I56563	frazzled gene prot
37	81	6.5	1375	2 T13822	frazzled gene prot
38	81	6.5	1526	2 T13823	cytochrome P450-11
39	80.5	6.5	566	2 T46159	CDO protein - rat
40	80.5	6.5	1256	2 T03096	hypothetical prote
41	80	6.4	335	2 T49145	RNA binding protei
42	80	6.4	703	2 T41065	cytokine receptor
43	79.5	6.4	359	2 JC7280	CDO protein - huma
44	79.5	6.4	1240	2 T03097	protein H19M22.1
45	79	6.4	1825	2 C88400	

ALIGNMENTS

RESULT 1

A49667  
interleukin-10 receptor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 28-Jul-2000  
C/Accession: A49667  
R;Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazar, J.F.; Moore, K.W.  
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993  
A>Title: A receptor for interleukin 10 is related to interferon receptors.  
A/Reference number: A49667; MUID:94068585; PMID:8248239  
A/Accession: A49667  
A/Status: Preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-575 <RES>  
A/Cross-references: GB:L12120; NID:G437615; PIDN:AAA16156.1; PID:G437616  
C/Genetics:  
A/Gene: IL10R  
C/Superfamily: interleukin-10 receptor IL10R  
C/Keywords: cytokine receptor

Query Match	14.0%;	Score	174.5;	DB 2;	Length	575;
Best Local Similarity	29.6%;	Pred. No.	9.1e-09;			
Matches	73;	Conservative	35;	Mismatches	92;	Indels 47; Gaps 15;
QY	7	LGLLLILSSATEIQPARVSI--TPQKVFQSRNFHNLHMQAGSSLP--SNNSTYFYQY	63			
Db	5	LLPFLVTISLSLEFIAYGTLPSPSYVWFARFFOHLHWK---PIPNQSESTYFEVAL	61			
QY	64	KMYGQSQWEDKVDCHGTTALFCDLTNETLDPYELYYG---RVMTACAGRHSATRT-PRP	119			
Db	62	KQYGNSTWMDIHICRAQALSCLDTFTLDLYHRSYGYRARVRAVDNSQYSNWTITTRF	121			
QY	120	TPWETKLDPPVVTITRYNASLVL-----LRPELPNRNQSGKNASMETIYGYLVY--	170			
Db	122	T-----VDEVILTVDVSV--TLKAMDGIYGTIHPPR-PTITPAGDE-----YEQVFKD	166			
QY	171	-RVFTINNSLEKEQKAYEGTORAVE-----IEGLIPHSYSYCVVAEMQPMFDRSPR---S	222			
Db	167	LAVYKI--SIRFSELKNATKRVKQETFTLTPIGVKRFV---KVLPIRTERINKAWS	221			

RESULT 2

I56215  
interleukin-10 receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 28-Jul-2000  
C/Accession: I56215  
R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.

J. Immunol. 152, 1821-1829, 1994  
A>Title: Expression cloning and characterization of a human IL-10 receptor.  
A/Reference number: 156215; MUID:94165477; PMID:8120391  
A/Accession: J56215  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-578 <RES>  
A/Cross-references: EMBL:U00672; NID:9482802; PIDN:AAAL7896.1; PID:9482803  
C/Genetics:  
A/Map position: 11Q23.3-11Q23.3  
C/Superfamily: interleukin-10 receptor IL10R  
C/Keywords: cytokine receptor

Query Match 14.0%; Score 174.5; DB 2; Length 578;  
Best Local Similarity 28.7%; Pred. No. 9.2e-09;  
Matches 72; Conservative 37; Mismatches 95; Indels 47; Gaps 15;

QY 1 MNPKHLLGLLILLS-----SATEIQPARVSLTPQKVRQSRNFHNLHQAQSSLP 53  
DB 1 MNP-CLVLLAALLSLRGLSDAHGTELP-----SPPSVWEAEFFHHILHW---TTP 49

QY 54 --SNNSIYVQVMYQSQWEDKVDGTTALFCDLTNETLDPYEL--YGRVMTACAGR 109  
DB 50 NOSESTCYEVALRYGIESWNSISNC--SQTLSYDLTAVTLDYHNSGYRVRVADGSR 107

QY 110 HSAWTRT-PRFTPWMTKLDPPVVTITRVNASLR--VLLRPPPELNRNOSGKNASMETYY 166  
DB 108 HSNWTVNTRFS-----VDEVLTVGSVNLHNGFILGKQLPRPKMAPANDYEIF 161

QY 167 GLVYRVFTINNSLEKEQAYEQTAVERTEGLIPHS-----YCVVAEMYQPMFRRSR 221  
DB 162 S-HFREYEI--AIRKVPNGFTTHKKVGHENFSLTSGEVGFVCV---QVKPSVASRSNK 215

QY 222 ---SKERCVHI 229  
DB 216 GMSKCECISL 226

RESULT 3  
JC6311  
C/Species: Mus musculus (house mouse)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000  
R/Gibbs, V.C.; Pennica, D.  
Gene 186, 97-101, 1997  
A/Title: CRF2-4: isolation of cDNA clones encoding the human and mouse proteins.  
A/Reference number: JC6311; MUID:97199375; PMID:9047351  
A/Accession: JC6311  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-349 <GIB>  
A/Cross-references: GB:U53696

Query Match 13.9%; Score 173; DB 2; Length 349;  
Best Local Similarity 27.8%; Pred. No. 6.7e-09;  
Matches 64; Conservative 32; Mismatches 94; Indels 40; Gaps 12;

QY 6 CLIGLL--IILLSSATEIQPARVSLTPQKVRQSRNFHNLHQAQSSLPNNVYFVQY 63  
DB 4 CVAGLWGLFLVPALGMIPP-----PEKVRMNSVNFKNILOVEV-PAPFKNTLFTAQY 56

QY 64 KMYQSQWEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGRHSATWTRPTPW 123  
DB 57 ESRASFQ----DHCKRTASTQCDFSH--LSKYGDYIVRVRAELADEHSWNV--RFCPVE 109

QY 124 ETKLDPVVTITRVNASLRVLLRPPPELNRNOSG--KNASMETYYGLVYRV-FTINNSL 180  
DB 110 DTIIGPEMQIESLAESLELRFAPQIENEPETWLKN-----IYDSWAYRVQVWKNGTNE 165

QY 181 KEQ--KAYEQTAVERTEGLIPHSYCV-----VAEMYQPMFDR 217

Db 166 KPOVSPYD-----SEVIRNLEFWTTCIQVQGLLDQNRIGWSEPICER 211

RESULT 4  
A31555  
interferon gamma receptor precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 23-Jul-1999  
C/Accession: A31555  
R/Aguet, M.; Dembic, Z.; Merlin, G.  
Cell 55, 273-280, 1988  
A/Title: Molecular cloning and expression of the human interferon-gamma receptor.  
A/Reference number: A31555; MUID:89003065; PMID:2971451  
A/Accession: A31555  
A/Molecule type: mRNA  
A/Residues: 1-489 <AGU>  
A/Cross-references: GB:J03143; NID:gl84650; PIDN:AAAS2731.1; PID:g306915  
C/Genetics:  
A/Map position: 6q23-6q24  
C/Superfamily: interferon gamma receptor  
C/Keywords: cytokine receptor; transmembrane protein

Query Match 13.3%; Score 165.5; DB 2; Length 489;  
Best Local Similarity 24.6%; Pred. No. 5.5e-08;  
Matches 60; Conservative 47; Mismatches 108; Indels 29; Gaps 10;

QY 7 LLGLLIILLSSATEIQPARVSL-----TPQKVRQSRNFHNLHW--QAQSLPSNNSI 58  
DB 3 LLFLLPLVMGVRAEAGTADLGPSSVPFTNTVIESYNNPIVYWEYQIMPOVP---V 58

QY 59 YFVQYKMYG--QSQWEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGRHSATWTR 116  
DB 59 FTVEVKNYGVKNSWIDA--CINISHHYCNISDHVGPSPNSLWVRVKARVGQKESAYAKS 116

QY 117 PRFTPWMTKLDPPVVTITRVNASLRV--VLLRPPPELNRNOSGKNASME--TYGLVYRVFT 174  
DB 117 EEFVAVCRDGRIGIPPKLDIRKEKQIMIDIFHPBSVFNVDGEQVDYDPTTCIRVNVYV 176

QY 175 INNSLEKEQAYEQTAVERTEGLIP-----HSSYCVVAEMYQPMFDRRSPSKER 225  
DB 177 RMNGSEIQYKIL--TKEDDCDEIQQLAIPVSSLNSQYCVSAEGLVHWGVVTEKSEV 234

QY 226 CVHI 229  
DB 235 CITI 238

RESULT 5  
A47003  
cytokine receptor family class II protein CRF2-4 precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 01-Dec-2000  
C/Accession: A47003; G01418  
R/Lutfalla, G.; Gardiner, K.; Uze, G.  
Genomics 16, 366-373, 1993  
A/Title: A new member of the cytokine receptor gene family maps on chromosome 21 at les;  
A/Reference number: A47003; MUID:93300510; PMID:8314576  
A/Accession: A47003  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-325 <LUT>  
A/Cross-references: GB:217227; NID:g3933378; PIDN:CAA78933.1; PID:g9393379  
R/Lutfalla, G.  
submitted to the EMBL Data Library, April 1994  
A/Reference number: G06935  
A/Accession: G01418  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-123 'D', 125-268 'VGRME' <LUT>  
A/Cross-references: EMBL:U08986; NID:g571295; PID:g571296





```
A;Molecule type: DNA
A;Residues: 473-590 <RE7>
A;Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:9510265
C;Genetics:
A;Gene: IFNAR
A;Introns: 177/3; 331/1
A;Keywords: cytokine receptor; transmembrane protein

Query Match 11.3%; Score 140; DB 2; Length 590;
Best Local Similarity 19.8%; Pred. No. 2.1e-05;
Matches 44; Conservative 49; Mismatches 113; Indels 16; Gaps 6;

QY 12 ILLSSATEIQPARVS-----LTPQKRVQSRNFHILHWQA-GSSLPSNNSIYFVQKMY 66
DB 10 LVLVAGAPWFLPSAAGGNLKPENIDYIIDDNYTLKWSHGSGMS--VTFSAEYRTK 67
QY 67 QSQWEDKVDQWGTALFCDLTNETLDPYELYYGRVMTACAGRHSAMTRTPRFFPWMTK 126
DB 68 DEAKWLKVPQCHITTKCEFSLLDTNVIYKQFRVRAEBCNSTSSWNEVDPPFFITYAH 127
QY 127 LDDPVVITRNVASLRVLLRPELPNRSQKNASME-TYYGLVYRVFTINNSLEKQKA 185
DB 128 MSPPEVLEAEADKAILVHISPP-----QDDGNMWALEKPSFYTRTWQKSSS---DKKT 179
QY 186 YEGTQRAVEIEGLPHSSVCYVAEMYYQMPDRRSPRSKERCY 227
DB 180 INSTYYVEKIPPELLPETTYCLEVKAHPSLKXHSNYSTVQCI 221

RESULT 10
KPM53
tissue factor precursor - mouse
N;Alternate names: coagulation factor III
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
R;Accession: A32318; A39046
R;Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
Mol. Cell. Biol. 9, 2567-2573, 1989
A;Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein ho
A;Reference number: A32318; MUID:89343974; PMID:2761539
A;Accession: A32318
A;Molecule type: mRNA
A;Residues: 1-294 <HAR>
A;Cross-references: GB:M26071; NID:G201924; PIDN:AAA40414.1; PID:G201925
R;Ranganathan, G.; Blatti, S.P.; Subramaniam, M.; Pass, D.N.; Mithle, N.J.; Getz, M.J.
J. Biol. Chem. 266, 496-501, 1991
A;Title: Cloning of murine tissue factor and regulation of gene expression by transformi
A;Reference number: A39046; MUID:91093171; PMID:1985911
A;Accession: A39046
A;Molecule type: mRNA
A;Residues: 1-25, '1', 27-294 <RAN>
A;Cross-references: GB:M57896; GB:J05713; NID:G201926; PIDN:AAA63400.1; PID:G201927
A;Note: 26-Thr was also found
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;30-294/Product: tissue factor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;252-274/Domain: transmembrane #status predicted <TMM>
F;37-57, 169, 200/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;75-83, 218-241/Disulfide bonds: #status predicted
F;7275/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 11.2%; Score 138.5; DB 1; Length 294;
Best Local Similarity 23.6%; Pred. No. 1.2e-05;
Matches 60; Conservative 39; Mismatches 90; Indels 65; Gaps 12;

QY 8 IGLILLSSATEIQPARVSLTPQKRVQSRNFHILHWQA-GSSLPSNNSIYFVQKMY 67
DB 18 LGCLLLQVTAGAGIPEKAFNLT-----WISTDFKTIIEWQP-----KPTNYTYTVOISDRS 68

A;Molecule type: DNA
A;Residues: 473-590 <RE7>
A;Cross-references: EMBL:U06244; NID:9497114; PIDN:AAA65008.1; PID:9510265
C;Genetics:
A;Gene: IFNAR
A;Introns: 177/3; 331/1
A;Keywords: cytokine receptor; transmembrane protein

Query Match 11.3%; Score 140; DB 2; Length 590;
Best Local Similarity 19.8%; Pred. No. 2.1e-05;
Matches 44; Conservative 49; Mismatches 113; Indels 16; Gaps 6;

QY 12 ILLSSATEIQPARVS-----LTPQKRVQSRNFHILHWQA-GSSLPSNNSIYFVQKMY 66
DB 10 LVLVAGAPWFLPSAAGGNLKPENIDYIIDDNYTLKWSHGSGMS--VTFSAEYRTK 67
QY 67 QSQWEDKVDQWGTALFCDLTNETLDPYELYYGRVMTACAGRHSAMTRTPRFFPWMTK 126
DB 68 DEAKWLKVPQCHITTKCEFSLLDTNVIYKQFRVRAEBCNSTSSWNEVDPPFFITYAH 127
QY 127 LDDPVVITRNVASLRVLLRPELPNRSQKNASME-TYYGLVYRVFTINNSLEKQKA 185
DB 128 MSPPEVLEAEADKAILVHISPP-----QDDGNMWALEKPSFYTRTWQKSSS---DKKT 179
QY 186 YEGTQRAVEIEGLPHSSVCYVAEMYYQMPDRRSPRSKERCY 227
DB 180 INSTYYVEKIPPELLPETTYCLEVKAHPSLKXHSNYSTVQCI 221

RESULT 11
A34368
interferon gamma receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 23-Jul-1999
C;Accession: A34368; A34423; A34508; A36224; I48941
R;Kumar, C.S.; Muthukumar, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.; Mariano, T.M.; Pestka,
J. Biol. Chem. 264, 17939-17946, 1989
A;Title: Molecular characterization of the murine interferon gamma receptor cDNA.
A;Reference number: A34368; MUID:90036866; PMID:2530216
A;Accession: A34368
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 <KUM>
A;Cross-references: GB:M25764; NID:G197962; PIDN:AAA39177.1; PID:G303933
R;Cofano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Appella, E.
J. Biol. Chem. 265, 4064-4071, 1990
A;Title: Affinity purification, peptide analysis, and cDNA sequence of the mouse interfe
A;Reference number: A35468; MUID:90154099; PMID:2137461
A;Accession: A35468
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 <COF>
A;Cross-references: GB:J05265; NID:G197964; PIDN:AAA39178.1; PID:G303934
R;Gray, P.W.; Leong, S.; Pennie, E.H.; Farrar, M.A.; Pingel, J.T.; Fernandez-Luna, J.; S
Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989
A;Title: Cloning and expression of the cDNA for the murine interferon gamma receptor.
A;Reference number: A34423; MUID:90046824; PMID:2530582
A;Accession: A34423
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-94, 'E', '96-477 <GRA>
A;Cross-references: GB:M26711; NID:G194126; PIDN:AAA37896.1; PID:G303930
R;Hemmi, S.; Peghini, P.; Metzler, M.; Merlin, G.; Dembic, Z.; Aguet, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989
A;Title: Cloning of murine interferon gamma receptor cDNA: expression in human cells med
A;Reference number: A34508; MUID:90099370; PMID:2532365
A;Accession: A34508
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-94, 'E', '96-477 <HEM>
A;Cross-references: GB:M28233; NID:G194131; PIDN:AAA37898.1; PID:G303931
R;Munro, S.; Maniatis, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
A;Title: Expression cloning of the murine interferon gamma receptor cDNA.
A;Reference number: A36224; MUID:90083245; PMID:2531896
A;Accession: A36224
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-477 <MUN>
A;Cross-references: GB:M28995; NID:G194123; PIDN:AAA37895.1; PID:G3039329
R;Raval, P.; Obici, S.; Russell, S.W.; Murphy, W.J.
Gene 154, 219-223, 1995
A;Title: Characterization of the 5' flanking region and gene encoding the mouse interfer
A;Reference number: I48941; MUID:95197006; PMID:7890167
A;Accession: I48941
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Query Match	5.5%	Score	1.000000	Length	100
Best Local Similarity	23.7%	Pred. No.	0.00039		
Matches	57	Conservative	42	Mismatches	97
Indels	45	Gaps	11		









Db 5 LLPFLVITSSLSLEFIAYGTETLSPSYWFEARFQHLHWK---PIPNQSESTYFEVAL 61  
QY 64 KMYGOSQWEDKVDGTTALFCDLTNETLDPYELYYG---RVMTACAGRHSAWTRT-PRF 119  
Db 62 KOYGNSTWHDHICRKAQALSCDLTTFILDYHRSYGYRVARVDNSQYSNWTTTETRF 121  
QY 120 TPWWTETKLDPPVWTTTRVNASLRLV-----LRPELPNRSQGNKASMTYGLVY-- 170  
Db 122 T-----VDEVLTVDVSV--TLKAMDGIHYGTIHPPR-FTITPAGDE-----YEQVFKD 166  
QY 171 -RVFTINNSLEKEQKAYEGTORAVE-----IEGLPHSSVCVVVAEYQPMFRRGRPR---S 222  
Db 167 LAVYKI--SIRFESLKNATKVKQETTLTVPVGRKFCV---KVLPRLESRLINKAENS 221  
QY 223 KERCVHI 229  
Db 222 ERQCLLI 228

RESULT 2  
ID IL10R HUMAN STANDARD; PRT; 578 AA.  
AC Q13651;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1).  
GN IL10RA OR IL10R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphoma;  
RX MEDLINE=94165477; PubMed=8120391;  
RA Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;  
RT "Expression cloning and characterization of a human IL-10 receptor.";  
RL J. Immunol. 152:1821-1829(1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANTS VAL-61; ILE-113; GLY-159; GLN-212;  
RP AEG-351 AND LEU-420.  
RA Rieder M.J., Hastings N.C., Arnel T.Z., Carrington D.P., Ozuna M.,  
RA Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Receptor for IL-10; binds IL-10 with a high affinity.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Spleen, thymus, and PBMC. Weak expression in  
pancreas, skeletal muscle, brain, heart, and kidney. Placenta,

CC lung, and liver showed intermediate levels. Monocytes, B cells,  
CC large granular lymphocytes, and T cells express high levels.  
CC -!- SIMILARITY: Belongs to the type II cytokine family of receptors.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: U00672; AAA17896.1; --  
CC EMBL: AV195619; AAN86349.1; --  
CC EMBL: BC028082; AAN828082.1; --  
CC PIR: I56215; I56215.  
CC PDB: 1J7V; 19-SEP-01.  
CC PDB: 1LQS; 17-JUL-02.  
CC Genes: HGNC:5964; IL10RA.  
CC MIM: 146933; --  
CC GO: GO:0005886; Cytoplasmic membrane; TAS.  
CC GO: GO:0004920; Finterleukin-10 receptor activity; TAS.  
CC GO: GO:0004872; Finterleukin-10 receptor activity; TAS.  
CC KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;  
KW 3D-structure.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 578 INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.  
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 236 256 POTENTIAL.  
FT DOMAIN 257 578 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 202 223 POTENTIAL.  
FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARIANT 61 61 L -> V. /FTID=VAR\_016294.  
FT VARIANT 113 113 V -> I. /FTID=VAR\_016295.  
FT VARIANT 159 159 S -> G. /FTID=VAR\_016296.  
FT VARIANT 212 212 R -> Q. /FTID=VAR\_016297.  
FT VARIANT 351 351 G -> R. /FTID=VAR\_016298.  
FT VARIANT 420 420 S -> L. /FTID=VAR\_016299.  
FT SEQUENCE 578 AA; 62903 MW; EE1B29064338157C CRC64;  
SQ  
Query Match 14.0%; Score 174.5; DB 1; Length 578;  
Best Local Similarity 28.7%; Pred. No. 8e-09;  
Matches 72; Conservative 37; Mismatches 95; Indels 47; Gaps 15;  
QY 1 MPPGHCLGLLIILLS-----SATEIQARVSLTPQKRVQSRNFHILHWQAGSSLP 53  
DB 1 MLP--CLVVLAAALLSLRLGSDAHGTELP-----SPPSWFEAEFFHILHW---TPIP 49  
QY 54 --SNNSIFYVOYKMGQSQWEDKVDGTTALFCDLTNETLDPYEL--YGRVMTACGR 109  
DB 50 NQSESTCYEALLRYGIESWNSISNC--SQTLSYDLTAVTLDLYHNGYRVARVVDGSR 107  
QY 110 HSAWTRT-PRFTPMWETKLDPPVWTTTRVNASLR--VLLRPPELPNRSQGNKASMETTY 166  
DB 108 HSNMTVTNTAFS-----VDEVLTGVSVNLETHNGFGLKQLPRPKMAPANDTYESIF 161  
QY 167 GLVYRVFTTINNSLEKEQKAYEGTORAVEIEGLPHSS-----YCVVAEMVQPMFDRSPR 221  
DB 162 S-HPREVEI--AIRKVPQNTFTTHKKVKNHENFSLTSGEVGEFCV---QVKPSVASRSNK 215  
QY 222 ---SKERCVHI 229

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2b 216 GWSKEECISL 226
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ID _10S_MOUSE STANDARD; PRT; 349 AA.
AC Q61190;
JT 16-OCT-2001 (Rel. 40, Created)
JT 16-OCT-2001 (Rel. 40, Last sequence update)
JT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE (Cytokine receptor class-II CRF2-4).
IN IL10RB OR CRFB4.
IN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9719375; PubMed=9047351;
XA Gibbs V.C., Pennica D.;
YA "CRF2-4: isolation of cDNA clones encoding the human and mouse
  proteins.";
RL Gene 186:97-101 (1997).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=98130620; PubMed=9463407;
XA Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Bauer M.,
YA Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;
RT "The orphan receptor CRF2-4 is an essential subunit of the interleukin
  10 receptor.";
RL J. Exp. Med. 187:571-578 (1998).
TC -1- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain
  essential for the active IL10 receptor complex and to initiate
  IL10-induced signal transduction events.
TC -1- SUBCELLULAR LOCATION: Type I membrane protein.
TC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
TC -1- SIMILARITY: Contains 2 fibronectin type III domains.
TC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
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  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
TC -----
TC EMBL: U53696; AAC53062.1; --
TC MGP; MG1:109380; I110rb.
TC DR GO: GO:0004920; F:interleukin-10 receptor activity; IMP.
TC DR GO: GO:0005515; F:protein binding; IPI.
TC DR InterPro: IPR000282; Cytok receptor_2.
TC DR InterPro: IPR008957; FN IIT-like.
TC DR InterPro: IPR003961; FN_IIT.
TC DR SMART: SM00060; FN3; 2.
TC KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL
FT CHAIN 1 19
FT DOMAIN 20 349 INTERLEUKIN-10 RECEPTOR BETA CHAIN.
FT TRANSMEM 20 220 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 221 241 POTENTIAL.
FT DOMAIN 242 349 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 113 205 FIBRONECTIN TYPE-III.
FT DISULFID 66 74 BY SIMILARITY.
FT DISULFID 188 209 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 349 AA; 39774 MW; 58BA4F6B86330A39 CRC64;
Query Match 13.9%; Score 173; DB 1; Length 349;
Best Local Similarity 27.8%; Pred. NO. 6e-09;

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Matches 64; Conservative 32; Mismatches 94; Indels 40; Gaps 12;

QY 6 CLLGL--IILLSSATEIQPARVSLTPQKVFQSRFNHILHWQAGSSLPNNNSIYFVQY 63

DB 4 CVAGWLGGLLVLPALGMIPP-----PEKVMNSVNFKNILQWEV-PAFPKTNLTFTAQY 56

QY 64 KMYGQSQWEDKVDGCGITALECDLTNETLDPYELLYGYGVMTACAGRHSANWTRTFPTPMW 123

DB 57 ESYRSFQ----DHCKRTASTQCFESH--LSKYGDYTVRVRAELADEHSEWNV-TFCEVE 109

QY 124 ETKLDPPPVVITRVNLSVLRPPPELPNNRQSG--KNASMETYYGLVYRV-FTNNLSLE 180

DB 110 DTIIIGPPPEQIESLAESLHLRFSAPQIENEPEWTCLKN----IYDSWAYRVQYKNGTNE 165

QY 161 KEQ--KAYEGTORAVEIEGLPHSSYCV-----VAENYQPMFDR 217

DB 166 KQVVSYPD----SEVLNLEPWTTCYIQVQGLDQNRGTGENSEPICER 211

RESULT 4

INGR HUMAN

ID INGR HUMAN STANDARD; PRT; 489 AA.

AC P15260;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Interferon-gamma receptor alpha chain precursor (CDw119).

GN IFNGR1

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89003065; PubMed=2971451;

RA Aguet M., Dembic Z., Merlin G.;

RT "Molecular cloning and expression of the human interferon-gamma

receptor.";

RL Cell 55:273-280 (1988).

RN [2]

RP SEQUENCE FROM N.A.

RA Phillimore B.;

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

[3]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).

RN [4]

RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.

RX MEDLINE=93183911; PubMed=8443182;

RA Strueber D., Friedlein A., Pountoulakis M., Lahm H.-W., Garotta G.;

RT "Alignment of disulfide bonds of the extracellular domain of the

interferon gamma receptor and investigation of their role in

RT biological activity.";  
RL Biochemistry 32:2423-2430(1993).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.  
RX MEDLINE=95342235; PubMed=7617032;  
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,  
RA Zaucodny P.J., Narula S.K.;  
RT "Crystal structure of a complex between interferon-gamma and its  
RT soluble high-affinity receptor.";  
RL Nature 376:230-235(1995).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 IN COMPLEX WITH  
RP ANTIBODY  
RX MEDLINE=98035727; PubMed=9367779;  
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,  
RA Winkler F.K., Robinson J.A.;  
RT "Neutralizing epitopes on the extracellular interferon gamma receptor  
RT (IFNGAMR) alpha-chain characterized by homolog scanning mutagenesis  
RT and X-ray crystal structure of the A6 fab-IFNGAMR1-108 complex.";  
RL J. Mol. Biol. 273:882-897(1997).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.  
RX MEDLINE=20444407; PubMed=10986460;  
RA Thiel D.J., le Du M.-H., Walter R.L., D'Arcy A., Chene C.,  
RA Fountoulakis M., Garotta G., Winkler F.K., Ballick S.E.;  
RT "Observation of an unexpected third receptor molecule in the crystal  
RT structure of human interferon-gamma receptor complex.";  
RL Structure 8:927-936(2000).  
CC -I- FUNCTION: Receptor for interferon gamma. Two receptors bind one  
CC interferon gamma dimer.  
CC -I- SUBUNIT: Monomer.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- PTM: Phosphorylated at Ser/Thr residues.  
CC -I- SIMILARITY: Belongs to the type II cytokine family of receptors.  
CC -I- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -I- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CDw119 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw119.htm".  
CC  
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CC  
CC EMBL; J03143; AAA52731.1; -;  
CC EMBL; AL050337; -; NOT ANNOTATED\_CDS.  
CC EMBL; BC008333; AAH05333.1; -;  
CC PIR; A31555; A31555.  
CC PDB; 1JRH; 25-MAR-98.  
CC PDB; 1FG9; 29-NOV-00.  
CC GlycoSuiteDB; P15260; -;  
CC Genew; HGNC:5439; IFNGR1.  
CC MIM; 107470; -;  
CC MIM; 209350; -;  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0003800; F:antiviral response protein activity; TAS.  
CC GO; GO:0004906; F:interferon-gamma receptor activity; TAS.  
CC GO; GO:0006955; P:immune response; TAS.  
CC GO; GO:0009619; P:resistance to pathogenic bacteria; TAS.  
CC GO; GO:0009615; P:response to viruses; TAS.  
CC GO; GO:0007165; P:signal transduction; TAS.  
CC InterPro; IPR00282; Cytok\_receptor\_2.  
CC InterPro; IPR008957; FN\_III-like.  
CC InterPro; IPR008355; IFNalpha.  
CC PRINTS; PR01777; INTERFERONGR.  
CC Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;  
KW Immunoglobulin domain; 3D-structure.  
FT SIGNAL 1 17  
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.  
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).  
FT

FT TRANSMEM 246 266 POTENTIAL. (POTENTIAL).  
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 77 85  
FT DISULFID 122 167  
FT DISULFID 195 200  
FT DISULFID 214 235  
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FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT STRAND 33 39  
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FT STRAND 58 65  
FT STRAND 74 80  
FT STRAND 84 86  
FT HELIX 88 90  
FT TURN 94 95  
FT STRAND 98 106  
FT TURN 107 108  
FT STRAND 109 110  
FT STRAND 114 115  
FT STRAND 119 119  
FT HELIX 121 124  
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FT STRAND 213 221  
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FT STRAND 227 227  
FT STRAND 234 236  
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Query Match 13.3%; Score 165.5; DB 1; Length 489;  
Best Local Similarity 24.8%; Pred. No. 4.7e-08;  
Matches 60; Conservative 47; Mismatches 108; Indels 29; Gaps 10;  
  
QY 7 LLGLLIILLSSATEIOPARVSL-----TPQKRVFOSRNFHILHW--QAGSLPNNISI 58  
DB 3 LLFLLPLVMQGSRAEMGTADLGPSSVPTPTNTVIESYNNNPVYWEYQIMPOVP----V 58  
QY 59 YFVQYKMYG--QSQWEDKVDWCWGTALFCDLTNETLDPYELYGRVMTACAGRHSAWTRT 116  
DB 59 FTVEVKYGVNSENWIDA--CINISHYCNISDHVGDPSNLSLWVRVKARVGQKESAYAKS 116  
QY 117 PRFTPPWETKLDPPVVTITRVNASLRV-LLRPPELPNRNQSNGKASNE-TYGLVTRVFT 174  
DB 117 BEPAVCDGKIGPPKLDIRKEEKQIMIDIFHPSPVFNVDQEQVDYDPTTCYIRVNVYV 176  
QY 175 INNSLEKEQKAYSGTQR-----AVEIEGLIP-----HSSYCVVAEMQPMFDRSPRKR 225  
DB 177 RMNGSEIQYKIL--TKEDDDCDEIQCOLAIPVSSLSNQYCVSAEGVLHWGVVTEKSEV 234  
QY 226 CVHI 229  
DB 235 CITI 238  
  
RESULT 5  
INR2 SHEEP  
ID INR2 SHEEP STANDARD; PRT; 536 AA.  
AC Q95207;  
DT 01-NOV-1997 (Rel. 35, Created)

15-JUL-1999 (Rel. 38, Last sequence update)  
15-MAR-2004 (Rel. 43, Last annotation update)  
Interferon-alpha/beta receptor beta chain precursor (IFN-alpha-REC)  
(Type I interferon receptor) (IFN-R) (Interferon alpha/beta receptor-  
2).  
DN IFNAR2 OR IFNARB.  
DS Ovis aries (Sheep).  
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
DC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;  
DC Bovidae; Caprinae; Ovis.  
DX NCBI\_TaxID=9940;  
RN [1]  
SEQUENCE FROM N.A.  
AC TISSUE=Endometrium;  
RX MEDLINE=98006426; PubMed=9349203;  
RA Han C.-S., Methalagan N., Klemann S.W., Roberts R.M.;  
RT "Molecular cloning of ovine and bovine type I interferon receptor  
subunits from uteri, and endometrial expression of messenger  
ribonucleic acid for ovine receptors during the estrous cycle and  
pregnancy.";  
RL Endocrinology 138:4757-4767(1997).  
CC -!- FUNCTION: Receptor for interferons alpha and beta. Probably  
involved in signal transduction by interacting with the tyrosine  
kinase, JAK1.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined except  
conceptus at day 15 of pregnancy.  
CC -!- SIMILARITY: Belongs to the type II cytokine family of receptors.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; U65979; AB84232.1; -  
CC InterPro; IPR000282; Cytok\_receptor\_2.  
CC InterPro; IPR008957; FN.III-like.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 536  
FT INTERFERON-ALPHA/BETA RECEPTOR BETA  
FT CHAIN  
FT DOMAIN 27 246  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 247 267  
FT POTENTIAL.  
FT DOMAIN 268 536  
FT CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 358 372  
FT 3 X 5 AA TANDEM REPEATS OF S-L-E-D-C.  
FT REPEAT 358 362  
FT REPEAT 363 367  
FT REPEAT 368 372  
FT REPEAT 368 372  
FT BY SIMILARITY.  
FT DISULFID 85 93  
FT BY SIMILARITY.  
FT CYS110 210 230  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 58 58  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 87 87  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 101 101  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 147 147  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 191 191  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT SEQUENCE 536 AA; 60260 MW; 1055F7D809545150 CRC64;  
Query Match 12.6%; Score 156; DB 1; Length 536;  
Best Local Similarity 26.9%; Pred. No. 4.2e-07;  
Matches 58; Conservative 39; Mismatches 73; Indels 46; Gaps 12;  
OY 32 KVFQSRPHILHWQAGSLPSNNISVFVCKMVG--QSQWED-KV--DCWGTALPCD 86  
DB 42 KMRP--RNQPSLSWEL-----KRSIVFTHYTWYIMSPDKMKVCKCINIRSFCD 94  
OY 87 LTNETLDYLYYGR-----VMTACAGRHSAWTRTPPTPWETKLDP--VVVIT 135  
DB 95 LTDVWNRDVMISQVGVRENNAVVSVMGSGFELASDKP-----LDPPKEIVDFT 145  
OY 136 -RVNASLVLRLPPLPRLPNRNSGKQASMETYVGLVRYFTINNSLEKEQAYGT---QR 191

146 NNISVNVKFRDSDRIPSEELQFLAIEEHAG-----NSVKHQPOITGNITENF 196  
OY 192 AVEIEGLIHSYCVVAEMQYQPMFDRSPRSKRCV 227  
DB 197 NYVIDKLIPNTNYC-ISVYFEPKPRKINRSLKCI 231  
RESULT 6  
TF\_CAVPO  
ID TF\_CAVPO STANDARD; PRT; 289 AA.  
AC Q9JLUS;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tissue factor precursor (TF) (Coagulation factor III).  
GN F3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=20206020; PubMed=10744153;  
RA Shi R.J., Li W.Z., Marder V.J., Sporn L.A.;  
RT "Cloning of guinea pig tissue factor cDNA: comparison of primary  
structure among six mammalian species.";  
RL Thromb. Haemost. 83:455-461(2000).  
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
CIRCULATING FACTOR VII OR VIIA. THE [TF.VIIA] COMPLEX ACTIVATES  
FACTORS IX OR X BY SPECIFIC LIMITED PROLYSIS. TF PLAYS A ROLE IN  
NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the tissue factor family.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; AF131949; AAF36523.1; -  
CC HSP; P13726; ITFH.  
CC InterPro; IPR000282; Cytok\_receptor\_2.  
CC InterPro; IPR008957; FN.III-like.  
CC InterPro; IPR001187; Tissue factor.  
CC Pfam; PF01108; Tissue fac; I.  
CC PRINTS; PR00346; TISSUEFACTOR.  
CC PROSITE; PS00621; TISSUE\_FACTOR; FALSE NEG.  
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
KW Palmitate.  
FT SIGNAL 1 32  
FT BY SIMILARITY.  
FT CHAIN 33 289  
FT TISSUE FACTOR.  
FT DOMAIN 33 247  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 248 268  
FT POTENTIAL.  
FT DOMAIN 269 289  
FT CYTOPLASMIC (POTENTIAL).  
FT SITE 44 46  
FT WKS MOTIF.  
FT SITE 75 77  
FT CARBOHYD 41 41  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 111 111  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 151 151  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 164 164  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT DISULFID 79 87  
FT BY SIMILARITY.  
FT DISULFID 213 236  
FT LIPID 271 271  
FT S-palmitoyl cysteine (By similarity).  
SQ SEQUENCE 289 AA; 32456 MW; 7AB97F8F58199FBI CRC64;  
Query Match 12.4%; Score 154; DB 1; Length 289;  
Best Local Similarity 25.4%; Pred. No. 3e-07;

Matches 60; Conservative 45; Mismatches 101; Indels 30; Gaps 13;  
QY 7 LGLLIILLSSATEIQPARVSLTPQKVFQSNFHNHLCAGSSLPNSNLSIYVQVQMY 66  
DB 21 LGLWLVQVAGAEI-----PVKPNLTWKSTNFKTILEWE-----PKPINN-VYTVQI--- 68  
QY 67 GOSQWED-KVDCWGTALFCDLTNETL-DPVELYGRVMTACAG-----RHSAWTRTPRF 119  
DB 69 -STALEDNKSIKSIATATECDLTSEMAENVQTYLARIISLLPSTGFLSDAVYSNSPEF 127  
QY 120 TPWWTETKL-DPVTITRNASLRVLLPPELPNRSQGNKASMETIYG--LVTRVFTIN 176  
DB 128 TPYQETNLGQPKIESFKLVGTGLANTVTRDTQTLARS-NGTFLSLRDFGKLNQVLYYWR 186  
QY 177 NLEKEQKAYEQTOR-AVEIEGLIHPSSYCVVAENVQVP--MFDPRSRSKERCYVHI 229  
DB 187 SSTTGKTKTANTWNEFLIDVD---KQDYCFPVQAVIPSRKDNKSPSITVCIHL 239  
RESULT 7  
ID \_T10S HUMAN STANDARD; PRT; 325 AA.  
AC Q08334;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)  
DE (Cytokine receptor class-II CRF2-4).  
GN IL10RB OR CRFB4  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Petal brain;  
RX MEDLINE=93300510; PubMed=83144576;  
RA Lutfalla G, Gardiner K, Uze G;  
RT "A new member of the cytokine receptor gene family maps on chromosome  
RT 21 at less than 35 kb from IFNAR.";  
RL Genomics 16:366-373(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96054036; PubMed=7563119;  
RA Lutfalla G, McInnis M.G., Antonarakis S.E., Uze G;  
RT "Structure of the human CRFB4 gene: comparison with its IFNAR  
RT neighbor.";  
RL J. Mol. Evol. 41:338-344(1995).  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=97459974; PubMed=9312047;  
RA Korten S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,  
RA Pestka S.;  
RT Identification and functional characterization of a second chain of  
RT the interleukin-10 receptor complex.";  
RL EMO J. 16:5894-5903(1997).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=10875937;  
RA Xie M.-H., Agarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,  
RA Wood W.I., Goddard A.D., Gurney A.L.;  
RT "Interleukin (IL)-22, a novel human cytokine that signals through the  
RT interferon receptor-related proteins CRF2-4 and IL-22R.";  
RL J. Biol. Chem. 275:31335-31339(2000).  
CC -1- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain  
CC essential for the active IL10 receptor complex and to initiate  
CC IL10-induced signal transduction events.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.  
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -----  
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CC EMBL; Z17227; CAA78933.1; -;  
CC EMBL; U08988; AAA86872.1; -;  
CC PIR; A47003; A47003.  
CC HSP; P13726; ITHF.  
CC Genew; HGNC:5965; IL10RB.  
DR MM; 123889; -;  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; TAS.  
DR GO; GO:0004920; F:interleukin-10 receptor activity; TAS.  
DR GO; GO:0004872; F:receptor activity; TAS.  
DR GO; GO:0006955; P:immune response; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR001187; Tissue\_factor.  
DR Pfam; PF01108; Tissue\_fac; I.  
DR SMART; SM00060; FN3\_2.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 325  
FT DOMAIN 20 220 INTERLEUKIN-10 RECEPTOR BETA CHAIN.  
FT TRANSMEM 221 242 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 243 325 POTENTIAL.  
FT DOMAIN 113 205 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 66 74 FIBRONECTIN TYPE-III.  
FT DISULFID 188 209 BY SIMILARITY.  
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 124 124 A -> D (IN REF. 2).  
FT CONFLICT 269 273 FLGHP -> VGRME (IN REF. 2).  
FT CONFLICT 274 325 MISSING (IN REF. 2).  
SQ SEQUENCE 325 AA; 37011 MW; 66706C79F814B23 CRC64;  
Query Match 12.3%; Score 153; DB 1; Length 325;  
Best Local Similarity 27.2%; Pred. No. 4.3e-07;  
Matches 61; Conservative 29; Mismatches 96; Indels 38; Gaps 10;  
QY 14 LLSSATEIQPARVSLTPQKVFQSNFHNHLCAGSSLPNSNLSIYVQVQMYGQSOWED 73  
DB 13 LLVSALGMVP-----PPENVNMSVNFKNILQWES-PAPAKGNLTFTAQYLSY--RIFQD 64  
QY 74 KVDWGTALFCDLTNETLDPYELYGRVMTACAGRHSAMTRTPRTPPWWTETKLDPPVVT 133  
DB 65 K-CWNTLTTCDFPS--SLSKYGDHILRVRAEFADEHSDWNI--TFCPVDDTIIGPFQM 119  
QY 134 ITRVNASLRVLLRPPELPNRSQSG--KNASMETIYGIVYVFTINNSLEKEQKAYEQTOR 191  
DB 120 VEVLADSLHMRFLAPKIENEYETWTKN-----VYNSWTINVQYWK-----NGTDE 165  
QY 192 AVEI-----EGLIPHSYCVVAENVQVPMDRRSPRSKERC 226  
DB 166 KFOITPQYDFEVLNLEWITTCYQVGRGFLPDRNKAGWSEPV 209  
RESULT 8  
ID \_TF BOVIN STANDARD; PRT; 292 AA.  
AC P30931;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tissue factor precursor (TF) (Coagulation factor III).  
GN F3.

OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Adrenal gland;  
RX MEDLINE=92109720; PubMed=1764065;  
RA Takayenoki Y., Muta T., Miyata T., Iwanaga S.;  
RT "cDNA and amino acid sequences of bovine tissue factor.";  
RL Biochem. Biophys. Res. Commun. 181:1145-1150(1991).  
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
CC CIRCULATING FACTOR VII OR VITA. THE [TF:VIA] COMPLEX ACTIVATES  
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the tissue factor family.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; S74147; AAB20755.1; --  
DR PIR: JQ1319; KFB03.  
DR HSSP: P24055; 1A21.  
DR InterPro: IPR000282; Cytok receptor 2.  
DR InterPro: IPR009577; FN\_III-like.  
DR Pfam: PF01108; Tissue fac; 1.  
DR PRINTS: PR00346; TISSUEFACTOR.  
DR PROSITE: PS00621; TISSUE FACTOR; 1.  
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
KW Palmitate.  
FT SIGNAL 1 35  
FT CHAIN 36 292 TISSUE FACTOR.  
FT DOMAIN 36 248 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 249 271 POTENTIAL.  
FT DOMAIN 272 292 CYTOPLASMIC (POTENTIAL).  
FT SITE 46 48 WKS MOTIF.  
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DISULFID 81 89 BY SIMILARITY.  
FT DISULFID 215 238 BY SIMILARITY.  
FT LIPID 274 274 S-palmitoyl cysteine (By similarity).  
SQ SEQUENCE 292 AA; 32475 MW; 5E471D92BFBC163 CRC64;  
Query Match 12.1%; Score 150; DB 1; Length 292;  
Best Local Similarity 24.9%; Pred. No. 7.3e-07;  
Matches 60; Conservative 47; Mismatches 90; Indels 44; Gaps 13;  
7 LIGLILIL---LSSATEIOPARVSTPQKVFOSRNFHILHWAGSLPNNISYFVQY 63  
21 LFGVLVIOGAGVAGTVDV-----VVAINITKSNFKTILEWEP---KXINHVYTVQI 70  
64 KMYGQSQEDKVDCKGTTALFCDLNETL-DPYELLYGRVMTACGRHSA-----WTRTP 117  
71 SP-RLGNWKNK--CFYTTNTECDVTDEIKVNVRETYLARVLSYPADTSSSTVEPPFTNSP 127  
118 RPTPWETKLDPPVVTI-----TRVNASI---RVLLRPPE--LPENQSGKNASMETVYG 167  
128 EFTPLETNLNGOFTTQSEFQVGTCLNVTVQDARTLVANSAPLSLSDVFGKDLNLTLYW 187  
168 LVYRVFTINNSLEKSKQAYEGTQRAVEIGLPHSSYC--VVAENYQPMFDRRFSRsker 225  
188 KA-----SSGKKKATNTNGFLIDVD---KGENYCFHVQAVILSRVNVCKSPSPDIK 237

OY 226 C 226  
DB 238 C 238  
RESULT 9  
TF HUMAN  
ID TF HUMAN STANDARD; PRT; 295 AA.  
AC P13726;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tissue factor precursor (TF) (Coagulation factor III)  
DE (Thromboplastin) (CD142 antigen).  
GN F3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89247359; PubMed=2719931;  
RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;  
RT "Complete sequence of the human tissue factor gene, a highly  
RT regulated cellular receptor that initiates the coagulation protease  
RT cascade.";  
RL Biochemistry 28:1755-1762(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87260946; PubMed=3037536;  
RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,  
RA Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.;  
RT "Isolation of cDNA clones coding for human tissue factor: primary  
RT structure of the protein and cDNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87244317; PubMed=3297348;  
RA Morrissey J.H., Fakhrai H., Edgington T.S.;  
RT "Molecular cloning of the cDNA for tissue factor, the cellular  
RT receptor for the initiation of the coagulation protease cascade.";  
RL Cell 50:129-135(1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8050796; PubMed=2823875;  
RA Scarpati E.M., Wen D., Broze G.J. Jr., Milewich J.P.,  
RA Fliedermeyer R.R., Siegel N.R., Sadler J.E.;  
RT "Human tissue factor: cDNA sequence and chromosome localization of  
RT the gene.";  
RL Biochemistry 26:5234-5238(1987).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88100453; PubMed=3424286;  
RA Fisher K.L., Gorman C.M., Vehar G.A., O'Brien D.P., Lawn R.M.;  
RT "Cloning and expression of human tissue factor cDNA.";  
RL Thromb. Res. 48:89-99(1987).  
RN [6]  
RP SEQUENCE FROM N.A., AND VARIANTS ALA-36 AND VAL-145.  
RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
RA Rajkumar N., Toth S.J., Yi C., Nickerson D.A.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Collier R.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Ioshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RN [10]  
RN [11]  
RN [12]  
RN [13]  
RX MEDLINE=96175641; PubMed=8598903;  
RX MEDLINE=96190957; PubMed=8609606;  
RX Moller Y.A., Ullsch M.H., de Vos A.M.;  
RT "The crystal structure of the extracellular domain of human tissue  
RT factor refined to 1.7-A resolution.";  
RL J. Mol. Biol. 256:144-159(1996).  
RX MEDLINE=96175641; PubMed=8598903;  
RX Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
RA Konigsberg W.H., Nemerson Y., Kirchofer D.;  
RT "The crystal structure of the complex of blood coagulation factor  
RT VIIa with soluble tissue factor.";  
RL Nature 380:41-46(1996).  
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 37-242 IN COMPLEX WITH FVIIA.  
RX Zhang E., St Charles R., Tulinsky A.;  
RT "Structure of extracellular tissue factor complexed with factor VIIa  
RT inhibited with a BPTI mutant.";  
RL J. Mol. Biol. 285:2089-2104(1999).  
CC -I- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF  
CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1  
CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND  
CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE  
CC RESPONSE.  
CC -I- SIMILARITY: Belongs to the tissue factor family.  
CC -I- DATABASE: NAME=TF; NOTE=CD guide CD142 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd142.htm".  
-----  
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CC -----  
DR EMBL; J02931; AAA61150.1; -  
DR EMBL; M6553; AAA61151.1; -  
DR EMBL; J02846; AAA61152.1; -  
DR EMBL; M27436; AAA36734.1; -  
DR EMBL; A19048; AAA01438.1; -  
DR EMBL; AF540377; AAN01236.1; -  
DR EMBL; AL138758; CAC15961.1; -  
DR EMBL; BC011029; AAH11029.1; -  
DR F1; A43645; KFHU3.  
DR PDB; 1BOY; 10-JUN-96.  
DR PDB; 2HFT; 29-JAN-96.  
DR PDB; 1DAN; 04-SEP-97.  
DR PDB; 1AHW; 19-AUG-98.  
DR PDB; 1TFR; 19-AUG-98.  
DR PDB; 1FAK; 03-DEC-99.  
DR PDB; 1JPS; 18-DEC-02.  
DR Genew; HGNC:3541; F3.  
DR MIM; 134390; -  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0003801; F:blood coagulation factor activity; TAS.  
DR InterPro; IPR000282; Cytochrome c2.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR001187; Tissue factor.  
DR Pfam; PF01108; Tissue fac. I.  
DR PRINTS; PR00346; TISSUEFACTOR.  
DR PROSITE; PS00621; TISSUE\_FACTOR; 1.  
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
KW Palmitate; 3D-structure; Polymorphism.  
FT SIGNAL 1 32  
FT CHAIN 33 295 TISSUE FACTOR.  
FT DOMAIN 33 251 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 252 274 POTENTIAL.  
FT DOMAIN 275 295 CYTOPLASMIC (POTENTIAL).  
FT SITE 46 48 WKS MOTIF.  
FT SITE 77 79 WKS MOTIF.  
FT SITE 190 192 WKS MOTIF.  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DISULFID 81 89  
FT DISULFID 218 241  
FT LIPID 277 277  
FT VARIANT 36 36 S-palmitoyl cysteine.  
FT VARIANT 145 145 T -> A.  
FT VARIANT 163 163 /FTID=VAR\_014298.  
FT VARIANT 163 163 I -> V.  
FT VARIANT 163 163 /FTID=VAR\_014299.  
FT CONFLICT 260 260 R -> W (in dbSNP:5901).  
FT STRAND 42 49 /FTID=VAR\_012008.  
FT TURN 50 51 V -> A (IN REF. 4).  
FT STRAND 52 58  
FT STRAND 64 72  
FT TURN 73 74  
FT STRAND 78 84  
FT STRAND 88 90  
FT STRAND 92 95  
FT HELIX 96 98  
FT TURN 99 100  
FT STRAND 103 111  
Query Match 11.7%; Score 145.5; DB 1; Length 295;  
Best Local Similarity 26.1%; Pred. No. 2e-06;  
Matches 61; Conservative 38; Mismatches 90; Indels 45; Gaps 14;  
QY 16 SSATEIQARVSLPQKRFQSRNFHILHWQAGSSLPSSNNISYFYQYKMGQSQWEDKV 75  
DB 32 ASGTTNTVAANLIT-----WKSTNFKTILEWEP-----KPVNQVTVQIST-KSGDMKSK- 80  
QY 76 DCGTTTALFCDLTNETHL-DPVELYGVGMIAACAGR-----HSAWTRTPRTFPMWETK 126  
DB 81 -CFYTTDTECDLTDDEIVKDVVKQTYLAVRFSIPAGNVSTSGAGEPLYSFPTPILETN 139



QY 127 LDPVWTI-----TRVNASL---RVLLRPPELPRNOSGNASMETYVG--LVVRVFTIN 176  
Db 140 LGQFTIQSFQGVKVNVTVEDETLVR-----RNWT--FLSLRDVFGKDLIYLYYK 191  
QY 177 NSLEKEKAYEGTOR-AVEIEGLPHSYCVVAEMYOP--MFDRSRKRCV 227  
Db 192 SSSGKKTAKTNTNEFLIDVD---KGENYCFVSQVAVIPSRVTNRKSTDSPEVCM 242

RESULT 10  
TF\_RABIT  
ID TF\_RABIT STANDARD; PRT; 292 AA.  
AC P24055;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tissue factor precursor (TF) (Coagulation factor III).  
GN F3.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA MEDLINE=91200676; PubMed=1840552;  
RX Andrews B.S., Rehmtulla A., Fowler B.J., Edgington T.S., Mackman N.;  
RT "Conservation of tissue factor primary sequence among three mammalian  
RT species.";  
RL Gene 98:265-269(1991).  
RN [2]  
RP SEQUENCE OF 33-292 FROM N.A.  
RC STRAIN=New Zealand white; TISSUE=Brain;  
RX MEDLINE=92081032; PubMed=1746002;  
RA Pawashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.;  
RT "Molecular cloning, characterization and expression of cDNA for  
RT rabbit brain tissue factor.";  
RL Thromb. Haemost. 66:315-320(1991).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.  
RX MEDLINE=98266351; PubMed=9605315;  
RA Muller Y.A., Kelley R.F., de Vos A.M.;  
RT "Hinge bending within the cytokine receptor superfamily revealed by  
RT the 2.4 A crystal structure of the extracellular domain of rabbit  
RT tissue factor.";  
RL Protein Sci. 7:1106-1115(1998).  
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES  
CC FACTORS IX OR X BY SPECIFIC LIMITED PROLYSIS. TF PLAYS A ROLE IN  
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: BRAIN, HEART.  
CC -!- SIMILARITY: Belongs to the tissue factor family.  
CC  
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CC  
CC EMBL; M55390; AAA63469.1; -  
CC DR EMBL; X53521; CAA37597.1; -  
CC DR F01; J00441; KFRB3.  
CC DR F02; J00441; KFRB3.  
CC DR F03; J00441; KFRB3.  
CC DR F04; J00441; KFRB3.  
CC DR F05; J00441; KFRB3.  
CC DR F06; J00441; KFRB3.  
CC DR F07; J00441; KFRB3.  
CC DR F08; J00441; KFRB3.  
CC DR F09; J00441; KFRB3.  
CC DR F10; J00441; KFRB3.  
CC DR F11; J00441; KFRB3.  
CC DR F12; J00441; KFRB3.  
CC DR F13; J00441; KFRB3.  
CC DR F14; J00441; KFRB3.  
CC DR F15; J00441; KFRB3.  
CC DR F16; J00441; KFRB3.  
CC DR F17; J00441; KFRB3.  
CC DR F18; J00441; KFRB3.  
CC DR F19; J00441; KFRB3.  
CC DR F20; J00441; KFRB3.  
CC DR F21; J00441; KFRB3.  
CC DR F22; J00441; KFRB3.  
CC DR F23; J00441; KFRB3.  
CC DR F24; J00441; KFRB3.  
CC DR F25; J00441; KFRB3.  
CC DR F26; J00441; KFRB3.  
CC DR F27; J00441; KFRB3.  
CC DR F28; J00441; KFRB3.  
CC DR F29; J00441; KFRB3.  
CC DR F30; J00441; KFRB3.  
CC DR F31; J00441; KFRB3.  
CC DR F32; J00441; KFRB3.  
CC DR F33; J00441; KFRB3.  
CC DR F34; J00441; KFRB3.  
CC DR F35; J00441; KFRB3.  
CC DR F36; J00441; KFRB3.  
CC DR F37; J00441; KFRB3.  
CC DR F38; J00441; KFRB3.  
CC DR F39; J00441; KFRB3.  
CC DR F40; J00441; KFRB3.  
CC DR F41; J00441; KFRB3.  
CC DR F42; J00441; KFRB3.  
CC DR F43; J00441; KFRB3.  
CC DR F44; J00441; KFRB3.  
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CC DR F46; J00441; KFRB3.  
CC DR F47; J00441; KFRB3.  
CC DR F48; J00441; KFRB3.  
CC DR F49; J00441; KFRB3.  
CC DR F50; J00441; KFRB3.  
CC DR F51; J00441; KFRB3.  
CC DR F52; J00441; KFRB3.  
CC DR F53; J00441; KFRB3.  
CC DR F54; J00441; KFRB3.  
CC DR F55; J00441; KFRB3.  
CC DR F56; J00441; KFRB3.  
CC DR F57; J00441; KFRB3.  
CC DR F58; J00441; KFRB3.  
CC DR F59; J00441; KFRB3.  
CC DR F60; J00441; KFRB3.  
CC DR F61; J00441; KFRB3.  
CC DR F62; J00441; KFRB3.  
CC DR F63; J00441; KFRB3.  
CC DR F64; J00441; KFRB3.  
CC DR F65; J00441; KFRB3.  
CC DR F66; J00441; KFRB3.  
CC DR F67; J00441; KFRB3.  
CC DR F68; J00441; KFRB3.  
CC DR F69; J00441; KFRB3.  
CC DR F70; J00441; KFRB3.  
CC DR F71; J00441; KFRB3.  
CC DR F72; J00441; KFRB3.  
CC DR F73; J00441; KFRB3.  
CC DR F74; J00441; KFRB3.  
CC DR F75; J00441; KFRB3.  
CC DR F76; J00441; KFRB3.  
CC DR F77; J00441; KFRB3.  
CC DR F78; J00441; KFRB3.  
CC DR F79; J00441; KFRB3.  
CC DR F80; J00441; KFRB3.  
CC DR F81; J00441; KFRB3.  
CC DR F82; J00441; KFRB3.  
CC DR F83; J00441; KFRB3.  
CC DR F84; J00441; KFRB3.  
CC DR F85; J00441; KFRB3.  
CC DR F86; J00441; KFRB3.  
CC DR F87; J00441; KFRB3.  
CC DR F88; J00441; KFRB3.  
CC DR F89; J00441; KFRB3.  
CC DR F90; J00441; KFRB3.  
CC DR F91; J00441; KFRB3.  
CC DR F92; J00441; KFRB3.  
CC DR F93; J00441; KFRB3.  
CC DR F94; J00441; KFRB3.  
CC DR F95; J00441; KFRB3.  
CC DR F96; J00441; KFRB3.  
CC DR F97; J00441; KFRB3.  
CC DR F98; J00441; KFRB3.  
CC DR F99; J00441; KFRB3.  
CC DR F100; J00441; KFRB3.

DR PROSITE; PS00621; TISSUE FACTOR; 1.  
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
KW Palmitate; 3D-structure.  
FT SIGNAL 1 32  
FT CHAIN 33 292  
FT DOMAIN 251 271  
FT TRANSMEM 272 292  
FT CYTOPLASMIC (POTENTIAL).  
FT SITE 44 46  
FT SITE 75 77  
FT SITE 77 77  
FT CARBOHYD 41 41  
FT CARBOHYD 114 114  
FT CARBOHYD 154 154  
FT CARBOHYD 167 167  
FT CARBOHYD 182 182  
FT CARBOHYD 182 182  
FT DISULFID 79 87  
FT DISULFID 216 239  
FT LIPID 274 274  
FT STRAND 40 47  
FT TURN 48 49  
FT STRAND 50 56  
FT STRAND 62 69  
FT STRAND 76 82  
FT STRAND 86 88  
FT HELIX 90 93  
FT TURN 94 95  
FT TURN 97 98  
FT STRAND 101 109  
FT STRAND 126 126  
FT STRAND 130 130  
FT HELIX 132 135  
FT STRAND 137 137  
FT STRAND 143 149  
FT TURN 150 151  
FT STRAND 152 157  
FT STRAND 161 165  
FT STRAND 170 172  
FT HELIX 173 177  
FT HELIX 178 180  
FT STRAND 182 188  
FT STRAND 196 200  
FT STRAND 204 208  
FT TURN 211 212  
FT STRAND 216 222  
FT TURN 224 225  
FT STRAND 231 231  
FT STRAND 238 239  
SQ SEQUENCE 292 AA; 32738 MW; 4860A1CADBACCF71 CRC64;  
Query Match 11.8%; Score 144.5; DB 1; Length 292;  
Best Local Similarity 24.8%; Pred. No. 2.4e-06;  
Matches 61; Conservative 43; Mismatches 99; Indels 43; Gaps 13;  
QY 2 MPKHCLLGLILLSSATEIQPARVSLTPQKVRFSQSRNFHILHWQAGSSLPNNNSIYFV 61  
Db 16 VPYTVLLGWLAAQVAAADTTGAYNLT-----WKSTNFKTILEWEP---KSIDHVTV 66  
QY 62 QYKMYGOSQHEKVDWCGTTALFCDLTNETL-DFYELYGVRVMTACAGHSA----- 112  
Db 67 QISTRLN-WKSK--CFLTAETECDLTDEYVDVGQTYMARVLSYPARNGTTFGPPEPP 123  
QY 113 WTERETPTWETKLDPVVY-TITRVNASLRVLLRPE-LPNRNOS-----GKNASM 162  
Db 124 FRNSPETPFLDNLGQPIQSFQVGTKLNVQDARTLVRENGTFLSLRAVFGKDLNY 183  
QY 163 ETYVGLVYRVFTINNSLEKEQKAYEGTORAVEIEGLPHSSYCVVAEMYOPMDR--RSP 220  
Db 184 TLYY---WRA-----SSGKKTATTNTNEFLIDVD---KGENYCFVSQVAVIPSRKRCV 233  
QY 221 RSKERC 226  
Db 234 ESLTEC 239







QY 8 LGLILLSSATEIQPARVSLTPQKVRFSORNFHILHWQAGSSLPNSNYSYFVQYKMYG 67  
 DB 18 LCCLLLQVAGAGIEKARNLT-----WISDFFKILEWQP-----KPTNYTYTQISDES 68  
 QY 68 QSQWEDKVDGCTTALFCDLNETL-DPVELYGRVMT-----ACAGRUSA 112  
 DB 69 RN-WKNK--CFSTTDECDLTDIEIKVDVTWAEAKVLSVPRNSVHGDDQLVHGEPP 125  
 QY 113 WRTPTFTPTWETKLDPPV-----TITRVNASLRVLLRPPPLPNRN 154  
 DB 126 FTAPEKFLPYRTNLGQVIFQFEQDGRKLVVVKDSLTVKNGTFTLT-----RQ 177  
 QY 155 QSGKASMETYGLVYRVPTTINSLEKEQAYGTQRAVEIGLPHSSYC--VVAENYQ 212  
 DB 178 VFGKDLG---YIIIVRK---GSSTGKNTINTNEFSIDVEGV---SYCFFVQAMIFS 227  
 QY 213 PMFDRSPRSKERC 226  
 DB 228 RKTQNSPGSSVTC 241

## RESULT 14

INR1\_BOVIN STANDARD; PRT; 560 AA.  
 ID INR1\_BOVIN STANDARD; PRT; 560 AA.  
 AC Q04730;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
 GN IFNAR1 OR IFNAR.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RX MEDLINE=93076908; PubMed=1446745;  
 RA Mouchel-Vielh E, Lufalla G, Mogenssen K.E., Uze G;  
 RT "specific antiviral activities of the human alpha interferons are  
 determined at the level of receptor (IFNAR) structure."  
 RL FEBS Lett. 313:255-259(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93305725; PubMed=8318540;  
 RA Lim J.-K., Langer J.A.;  
 RT "cloning and characterization of a bovine alpha interferon receptor."  
 RL Biochim. Biophys. Acta 1173:314-319(1993).  
 CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
 CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
 CC including JAKs, TYK2, STAT proteins and IFNAR alpha- and beta-  
 CC subunits themselves.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the type II cytokine family of receptors.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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 CC -----  
 CC EMBL; X68443; CAA48484.1; -;  
 DR EMBL; L06320; AAA02571.1; -;  
 DR PIR; S27387; S27387.  
 DR InterPro; IPR000282; Cytok receptor\_2.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR001187; Tissue\_factor.

PFam; PF01108; Tissue\_fac; 1.  
 DR SMART; SM00060; FN3; 2.  
 KW Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 560  
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA  
 FT CHAIN.  
 FT DOMAIN 25 437  
 FT TRANSMEM 438 458  
 FT DOMAIN 459 560  
 FT DISULFID 76 84  
 FT DISULFID 199 220  
 FT CARBOHYD 47 47  
 FT CARBOHYD 55 55  
 FT CARBOHYD 85 85  
 FT CARBOHYD 109 109  
 FT CARBOHYD 172 172  
 FT CARBOHYD 254 254  
 FT CARBOHYD 313 313  
 FT CARBOHYD 377 377  
 FT CARBOHYD 434 434  
 FT CONFLICT 422 422  
 SQ SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;  
 Query Match: 10.8%; Score 134.5; DB 1; Length 560;  
 Best Local Similarity 23.8%; Pred. No. 4.8e-05;  
 Matches 45; Conservative 34; Mismatches 89; Indels 21; Gaps 7;  
 QY 29 TPQKVRFSORNFHILHWQAGSSLPNSNYSYFVQY-----KMYG--QSQWEDKVDGCT 80  
 DB 231 SPENIQINADNQIYVLKW-----DYPENATFOQWLRAFKKIPGNHSDKWKQIPNCENV 286  
 QY 81 TALFCDLNETLDPVELYGRVMTACAGRHSAWTRTPRTPMWETKLDPPVVTITRV-NA 139  
 DB 287 TSTHCYFPRE-VSSRGIIYVVRASNGNGTSFWSBEKEFNTEMTKTIIFPVISVKSVTDD 345  
 QY 140 SLRVLLRPPPLPNRQSGKASMETYGLVYRVPTTINSLEKEQAYGTQRAVEIGLI 199  
 DB 346 SLHVS-----GASEESENMSVNLPLYIYFIFWENTSNAERKYLEKRTNFI-PPDLK 398  
 QY 200 PHSSYCVVA 208  
 DB 399 PLTVYCVKA 407  
 RESULT 15  
 INR2\_BOVIN STANDARD; PRT; 530 AA.  
 ID INR2\_BOVIN STANDARD; PRT; 530 AA.  
 AC Q95141;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Interferon-alpha/beta receptor beta chain precursor (IFN-alpha-REC)  
 DE (Type I interferon receptor) (IFN-R) (interferon alpha/beta receptor-  
 DE 2).  
 GN IFNAR2 OR IFNARB.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=98006425; PubMed=9348203;  
 RA Han C.-S., Mathialagan N., Kiemann S.W., Roberts R.M.;  
 RT "Molecular cloning of ovine and bovine type I interferon receptor  
 RT subunits from uteri, and endometrial expression of messenger  
 RT ribonucleic acid for ovine receptors during the estrous cycle and  
 RT pregnancy."  
 RL Endocrinology 138:4757-4767(1997).  
 CC -!- FUNCTION: Receptor for interferons alpha and beta. Probably  
 CC involved in signal transduction by interacting with the tyrosine  
 CC kinase, JAK1.



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OM protein - protein search, using sw model

Run on: March 12, 2004, 15:56:12 ; Search time 45 Seconds  
(without alignments)  
1612.649 Million cell updates/sec

Title: US-10-090-365-48

Perfect score: 1242

Sequence: 1 MPPKCHLGLLILLSSATE.....YQPFDRSPRSKRCVHIP 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rviro:\*

16: sp\_bacteriapi:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	230	11 Q7TN15	Q7tn15 mus musculus
2	1231	99.1	230	11 Q80XF5	Q80xf5 mus musculus
3	1049	84.5	229	11 Q7TN14	Q7tn14 rattus norv
4	826.5	66.5	231	4 Q96A41	Q96a41 homo sapien
5	800.5	64.5	263	4 Q969J5	Q969j5 homo sapien
6	433.5	34.9	130	4 Q96QR0	Q96qr0 homo sapien
7	285.5	23.0	546	11 Q8BW64	Q8bw64 mus musculus
8	277	22.3	553	4 Q9UHE4	Q9uh4 homo sapien
9	277	22.3	553	4 Q96SH8	Q96sh8 homo sapien
10	263	21.2	581	11 Q80XZ4	Q80xz4 mus musculus
11	254	20.5	574	4 Q9N6P7	Q9n6p7 homo sapien
12	254	20.5	574	4 Q9HB22	Q9hb22 homo sapien
13	237.5	19.1	209	4 Q96SH7	Q96sh7 homo sapien
14	215	17.3	203	13 Q7ZT05	Q7zt05 tetraodon n
15	210.5	16.9	568	13 Q80OG1	Q80og1 tetraodon n
16	210.5	16.9	568	13 Q80OF7	Q80of7 tetraodon n

17	186	15.0	569	11 Q99ND6	Q99nd6 rattus norv
18	184.5	14.9	435	13 Q7ZT26	Q7zt26 tetraodon n
19	168	13.5	351	11 Q8VHM7	Q8vhm7 mus musculus
20	163.5	13.2	489	4 Q9BY69	Q9by69 homo sapien
21	158.5	12.8	569	13 Q9YHW0	Q9yhw0 gallus gall
22	156.5	12.6	341	13 Q9YGC8	Q9ygc8 gallus gall
23	155.5	12.5	442	13 Q9PVJ9	Q9pvj9 gallus gall
24	153	12.3	325	4 Q9BUU4	Q9buu4 homo sapien
25	152	12.2	336	13 Q800E8	Q800e8 tetraodon n
26	151	12.2	484	4 Q14936	Q14936 homo sapien
27	148	11.9	535	11 Q8CGK5	Q8cgg5 mus musculus
28	147	11.8	338	13 Q800G2	Q800g2 tetraodon n
29	145	11.7	508	13 Q9YHV9	Q9yvh9 gallus gall
30	143.5	11.6	211	4 Q8IZI7	Q8izi7 homo sapien
31	143.5	11.6	244	4 Q8IV66	Q8iv66 homo sapien
32	143.5	11.6	491	4 Q8IZI8	Q8izi8 homo sapien
33	143.5	11.6	520	4 Q8IU57	Q8iu57 homo sapien
34	143	11.5	508	13 Q9PVR0	Q9pvk0 gallus gall
35	140	11.3	590	11 Q80UR8	Q80ur8 mus musculus
36	140	11.3	590	11 Q80UJ3	Q80uj3 mus musculus
37	138.5	11.2	294	11 Q8R301	Q8r3l mus musculus
38	138.5	11.2	477	11 Q91Y85	Q9ly85 mus musculus
39	137.5	11.1	220	4 Q86SE7	Q86se7 homo sapien
40	137.5	11.1	238	4 Q86WH4	Q86wh4 homo sapien
41	134.5	10.8	464	11 Q9QZ62	Q9qz62 rattus norv
42	131	10.5	301	13 Q7ZT35	Q7zt35 tetraodon n
43	130.5	10.5	294	13 Q90W13	Q90w13 oncorhynch
44	123.5	9.9	239	4 Q15467	Q15467 homo sapien
45	123.5	9.9	331	4 Q9BUA0	Q9buao homo sapien

## ALIGNMENTS

### RESULT 1

Q7TN15 ID Q7TN15 PRELIMINARY; PRT; 230 AA.

AC Q7TN15; Q7TN15 (TREMREL. 25, Created)

DT 01-OCT-2003 (TREMREL. 25, Last sequence update)

DT 01-OCT-2003 (TREMREL. 25, Last annotation update)

DE Putative cytokine receptor family II soluble 1 precursor.

GN CRP2-S1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/c; TISSUE=Spleen;

RA Gruenberg B.H., Weiss B., Asadullah K., Sabat R.;

RT "Comparison of the human and murine IL-22BP gene leads to differences

RT in gene structure and expression."

RL Submitted (APR-2003) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AJ555484; CAD88474.1; ..

KW Receptor; Signal.

FT SIGNAL 1 18

FT CHAIN 19 230 putative cytokine receptor family II

SQ SEQUENCE 230 AA; 26612 MW; 9ABEB4EDFBAFC105 CRC64;

soluble 1.

Query Match 100.0%; Score 1242; DB 11; Length 230;

Best Local Similarity 100.0%; Pred. No. 5.5e-120;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPKCHLGLLILLSSATEIQPARVSLTPQKVFQSRNFNHLHWAGSLPNSNIYF 60

Db 1 MPPKCHLGLLILLSSATEIQPARVSLTPQKVFQSRNFNHLHWAGSLPNSNIYF 60

QY 61 VOYKMGQSQWEDKVDYCWGTTALFCDLTNETLDPYELYYGRVMTACGRHSAWTRTPFT 120

Db 61 VOYKMGQSQWEDKVDYCWGTTALFCDLTNETLDPYELYYGRVMTACGRHSAWTRTPFT 120

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QY 121 PWETKLDPPVVTITRVNASRLVLLRPPELNNQSGKNASMETYYGLVYRVFTINNSLE 180
DB 121 PWETKLDPPVVTITRVNASRLVLLRPPELNNQSGKNASMETYYGLVYRVFTINNSLE 180
QY 181 KEQKAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKERCVCVHP 230
DB 181 KEQKAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKERCVCVHP 230
RESULT 2
Q80XF5 PRELIMINARY; PRT; 230 AA.
AC Q80XF5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Interleukin 22 soluble receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=22586333; PubMed=12700595;
RA Wei C.C., Ho T.W., Liang W.G., Chen G.Y., Chang M.S.;
RT "Cloning and characterization of mouse IL-22 binding protein.";
RL Genes Immun. 4:204-211(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RA EMBL: AF493604; AAPI3730.1;
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain...); IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000282; Cytok receptor_2.
DR InterPro: IPR008957; FN_III-like.
KW Receptor.
SQ SEQUENCE 230 AA; 26589 MW; 9AEA29768A756A75 CRC64;
Query Match 99.18; Score 1231; DB 11; Length 230;
Best Local Similarity 99.18; Pred. No. 7.5e-119;
Matches 228; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MMPKHCLLGLLIISSATEIQPARVSLTPQKVFQSRNFHNLHQAGSSLPNNKIYF 60
DB 1 MMPKHCLLGLLIISSATEIQPARVSLTPQKVFQSRNFHNLHQAGSSLPNNKIYF 60
QY 61 VOYKYGQSQWEDKVCWGTTALFCDLTNETLDPYELYGRVMTACAGRHSAWTRTPRT 120
DB 61 VOYKYGQSQWEDKVCWGTTALFCDLTNETLDPYELYGRVMTACAGRHSAWTRTPRT 120
QY 121 PWETKLDPPVVTITRVNASRLVLLRPPELNNQSGKNASMETYYGLVYRVFTINNSLE 180
DB 121 PWETKLDPPVVTITRVNASRLVLLRPPELNNQSGKNASMETYYGLVYRVFTINNSLE 180
QY 181 KEQKAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKERCVCVHP 230
DB 181 KEQKAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKERCVCVHP 230
RESULT 3
Q7TN14 PRELIMINARY; PRT; 229 AA.
AC Q7TN14
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Interleukin 22 soluble receptor.
OS Cytokine receptor family II soluble 1.
GN CR22-S1.
OS Rattus norvegicus (Rat).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Spleen;
RA Gruenberg B.H., Weiss B., Asadullah K., Sabat R.;
RT "Comparison of the human and murine IL-22BP gene leads to differences
in gene structure and expression.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ555485; CAD88475.1;
KW Receptor; Signal.
FT SIGNAL 1 20
FT CHAIN 21 229 cytokine receptor family II soluble 1.
SQ SEQUENCE 229 AA; 26721 MW; 5CFDP37652A99365 CRC64;
Query Match 84.58; Score 1049; DB 11; Length 229;
Best Local Similarity 84.38; Pred. No. 4.8e-100;
Matches 193; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
QY 2 MPKCHCLLGLLIISSATEIQPARVSLTPQKVFQSRNFHNLHQAGSSLPNNKIYFV 61
DB 1 MPKCHCLLGLLIISSATEIQPARVSLTPQKVFQSRNFHNLHQAGSSLPNNKIYFV 60
QY 62 QYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYGRVMTACAGRHSAWTRTPRT 121
DB 61 QYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYGRVMTACAGRHSAWTRTPRT 120
QY 122 WNETKLDPPVVTITRVNASRLVLLRPPELNNQSGKNASMETYYGLVYRVFTINNSLEK 181
DB 122 WNETKLDPPVVTITRVNASRLVLLRPPELNNQSGKNASMETYYGLVYRVFTINNSLEK 180
QY 182 EQKAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKERCVCVHP 230
DB 182 EQKAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKERCVCVHP 229
RESULT 4
Q96A41 PRELIMINARY; PRT; 231 AA.
AC Q96A41
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Soluble cytokine class II receptor, short isoform precursor
(interleukin 22-binding protein CRF2-10) (Class II cytokine receptor)
DE (interleukin-22 binding protein).
GN CRF2-S1 OR IL22BP OR IL22RA2 OR IL-22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=21518574; PubMed=11607789;
RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,
Wolk K., Asadullah K., Sabat R.;
RT "A novel, soluble homologue of the human IL-10 receptor with
preferential expression in placenta.";
RL Genes Immun. 2:329-334(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mironchitschenko O.V., Esterova E.,
Dickensheets H., Donnelly R.P., Pestka S.;
RT "Identification, cloning, and characterization of a novel soluble
receptor that binds IL-22 and neutralizes its activity.";
RL J. Immunol. 166:7096-7103(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396522; PubMed=11481447;
RA Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,
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Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer S.,  
 Yao L., Whitmore T.E., Chandrasekhar Y., Grant F.J., Maurer M.,  
 Jelinek L., Storey H., Brander T., Hammond A., Topouzis S.,  
 Clegg C.H., Foster D.C.,  
 "A soluble class II cytokine receptor, IL-22RA2, is a naturally  
 occurring IL-22 antagonist.",  
 Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516 (2001).  
 [4]  
 SEQUENCE FROM N.A.  
 RP TISSUE=Breast;  
 RA Dumoulier L., Lejeune D., Renaud J.C.;  
 "Cloning and characterization of Interleukin-22 Binding Protein (IL-  
 22BP), a natural antagonist of IL-TIF/IL-22.",  
 Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ313161; CAC85634.1; -  
 DR EMBL: AY040566; AAK85714.1; -  
 DR EMBL: AY044429; AAK91775.1; -  
 DR EMBL: AJ297262; CAC83097.1; -  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR InterPro: IPR000282; Cytok receptor\_2.  
 DR InterPro: IPR008957; FN\_III-like.  
 KW Receptor; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 231 SOLUBLE CYTOKINE CLASS II RECEPTOR, SHORT  
 FT ISOFORM.  
 SQ SEQUENCE 231 AA; 26979 MW; 24A6912BFF75100F CRC64;  
 Query Match 66.5%; Score 826.5; DB 4; Length 231;  
 Best Local Similarity 66.7%; Pred. No. 4.7e-77;  
 Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;  
 QY 1 MNPXKCLLGLLI-ILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSNNSIY 59  
 DB 1 MNPXKCLLGLLI-ILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSNNSIY 60  
 QY 60 FVOYKMGQSQWEDKVCDCWGTALFCDLTTNETLPVELYGRVMTACAGRHSAWTRPRF 119  
 DB 61 FVOYKMGQSQWEDKVCDCWGTALFCDLTTNETLPVELYGRVMTACAGRHSAWTRPRF 120  
 QY 120 TPWNETKLDPPVITRVNASLRLRPPELPNRSQGNASMETYYGLVYRVFTINNSL 179  
 DB 121 TPWNETKLDPPVITRVNASLRLRPPELPNRSQGNASMETYYGLVYRVFTINNSL 180  
 QY 180 EKEQKAYEGTORAVEIEGLIPHSYCVVAEMYPMDRRSPRSKRCVHIP 230  
 DB 181 EKEQKAYEGTORAVEIEGLIPHSYCVVAEMYPMDRRSPRSKRCVHIP 231  
 RESULT 5  
 Q969J5 PRELIMINARY; PRT; 263 AA.  
 AC Q969J5  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Soluble cytokine class II receptor, long isoform precursor  
 DE (Interleukin 22-binding protein CRF2-10L).  
 GN CRF2-S1 OR IL22BP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=21518574; PubMed=11607789;  
 RA Gruenberg B.H., Schonenmeyer A., Weiss B., Toschi L., Kunz S.,  
 Wolk K., Asadullah K., Sabat R.;  
 "A novel, soluble homologue of the human IL-10 receptor with  
 preferential expression in placenta.",  
 Genes Immun. 2:329-334 (2001).  
 RL

[2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21286453; PubMed=11390454;  
 RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,  
 Dickensheets H., Donnelly R.P., Pestka S.;  
 "Identification, cloning, and characterization of a novel soluble  
 receptor that binds IL-22 and neutralizes its activity.",  
 J. Immunol. 166:7096-7103 (2001).  
 DR EMBL: AJ313162; CAC85635.1; -  
 DR EMBL: AY040567; AAK85715.1; -  
 DR Genew; HGNC:14901; IL22RA2.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR InterPro: IPR000282; Cytok receptor\_2.  
 DR InterPro: IPR008957; FN\_III-like.  
 KW Receptor; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 263 SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG  
 FT ISOFORM.  
 SQ SEQUENCE 263 AA; 30550 MW; C96EC5D78AC79B CRC64;  
 Query Match 64.5%; Score 800.5; DB 4; Length 263;  
 Best Local Similarity 58.6%; Pred. No. 2.7e-74;  
 Matches 154; Conservative 20; Mismatches 56; Indels 33; Gaps 2;  
 QY 1 MNPXKCLLGLLI-ILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSNNSIY 59  
 DB 1 MNPXKCLLGLLI-ILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSNNSIY 60  
 QY 60 FVOYKMGQSQWEDKVCDCWGTALFCDLTTNETLPVELYGRVMTACAGRHSAWTRPRF 87  
 DB 61 FVOYKMGQSQWEDKVCDCWGTALFCDLTTNETLPVELYGRVMTACAGRHSAWTRPRF 120  
 QY 88 TNETLDPVELYGRVMTACAGRHSAWTRPRTPWNETKLDPPVITRVNASLRLRP 147  
 DB 121 TSGETSDIQEPYGRVRAASAGSYSEMSMTPTPTWETKIDPPVNNITQVANGSLVLHA 180  
 QY 148 PELPNRSQGNASMETYYGLVYRVFTINNSLEKEQKAYEGTORAVEIEGLIPHSYCVV 207  
 DB 181 PNLPRYQKKNVSDYELLYRVFINNSLEKEQKAYEGTORAVEIEGLIPHSYCVV 240  
 QY 208 AEMYQPMFDRSPRSKRCVHIP 230  
 DB 241 ABTYQPMFDRSPRSKRCVHIP 263  
 RESULT 6  
 Q96QR0 PRELIMINARY; PRT; 130 AA.  
 AC Q96QR0  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Interleukin 22-binding protein CRF2-10S.  
 GN IL22BP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21286453; PubMed=11390454;  
 RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,  
 Dickensheets H., Donnelly R.P., Pestka S.;  
 "Identification, cloning, and characterization of a novel soluble  
 receptor that binds IL-22 and neutralizes its activity.",  
 J. Immunol. 166:7096-7103 (2001).  
 DR EMBL: AY040568; AAK85716.1; -  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR InterPro: IPR000282; Cytok receptor\_2.  
 DR InterPro: IPR008957; FN\_III-like.

C9UHF4	PRELIMINARY;	PRT;	553 AA.
C9UHF4			
AC	01-WA-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Class II cytokine receptor ZCYTOR7.		
GN	ZCYTOR7.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lok S., Kho C., Jeimberg A., Adams R., Whitmore T., Farrah T.,		
RA	O'Hara P.;		
RT	"Homo sapientis cytokine receptor homolog.";		
RRL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,		
RA	Martinez T., Hofman R., O'Hara P.;		
RA	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF184971; AAF01320.1; -		
DR	HSSP; P13726; 2HFT.		
DR	GeneW; HGNC:6003; IL2ORA.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0007536; F:blood coagulation; IEA.		
DR	InterPro; IPR000282; CytoC_receptor_2.		
DR	InterPro; IPR008957; FN III-like.		
DR	InterPro; IPR001187; Tissue_factor.		
KW	Pfam; PF01108; Tissue_fac; 1.		
KW	Receptor.		
SQ	SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;		
Query Match 22.3%; Score 277; DB 4; Length 553;			
Best Local Similarity 32.5%; Pred.No. 8.8e+20;			
Matches 65; Conservative 30; Mismatches 99; Indels 6; Gaps 3			
QY	30 POKRVFQRNFHNTHHQAGSSLPFNNSIYVQYKMGQSQWEDKVDGWTALFCDLTN 89		
Db	40 PANITFLSINMKNVLTWPPEGLGVKVTVTVQVFYIGKKLNKSECRNINRNYCDLSA 99		
QY	90 ETLDPIEYLRYGVMTACAGRHSATRTPTPHWEIKLDPDVVTITRVNASLVLLRPPE 149		
Db	100 ETSDDYEHOYAKVAIXMGTCKSKWAESGRFPYLETQIGEPFVALTTDSKSISVVLTAE 159		
QY	150 LPNRNQSGKNASMETYY-GLVRYVFTINNLSLEKEAKYEG--TQRAVEIEGIIPHSYCV 206		
Db	160 KWKRNPEPLPSVMQQIYSNLKNYVSVLNT--KSNRTWSQCVTNHTLVLTLEPNTLYVC 216		
QY	207 VAEMYQPMDFRSPRSKERC 226		
Db	217 HVSEFVGPPRRAPQFSEKQC 236		
RESULT 9			
Q96SH8	PRELIMINARY;	PRT;	553 AA.
ID	Q96SH8		
AC	Q96SH8;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	BA204P2.1.1 (Interleukin 20 receptor alpha, isoform 1).		
GN	IL20RA.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Griffiths C.;		



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RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL135902; CAC38375.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004896; F: hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0007596; P: blood coagulation; IEA.
DR GO: GO:000282; C: cytokine receptor_2.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF01108; Tissue_fac; I.
DR Receptor.
SQ SEQUENCE 553 AA; 62485 MW; D5C2621FDC848328 CRC64;

Query Match 22.3%; Score 277; DB 4; Length 553;
Best Local Similarity 32.5%; Pred. No. 8.8e-20;
Matches 65; Conservative 30; Mismatches 99; Indels 6; Gaps 3;

QY 30 PQKVFQSRNFHNLHWQAGSSLPNNISYFVQYKMGQSQWEDKVDGCTGTTALFCDLTN 89
DB 40 PANITFSLINKNVQLQWTPPEGLQGVKTYTVQYFIYQKKWLKNSCRNINRTYCDLSA 99
QY 90 ETLDPYELYYGRVMTACAGHSASWTRTPFTPMWETKLDPPVVTITRVNASLRVLLPPEL 149
DB 100 ETSYEHQYAKVAKAIMGKTKWAESGRFFYLETQIGPPEVALTTDEKSIISVLTAPE 159
QY 150 LPNRNQGKNSMETY-GLYRVFTTNNSLEKQKAYEG--TORAVEIEGLIPHSSYCV 206
DB 160 KWKRNPEPLPVMQOIVSNLKNVSVLNT---KSNRTWSQCVTNHTLVLTWLEPNTLYCV 216
QY 207 VAEYQPMFDRSPRSKERC 226
DB 217 HVESFVPGPPRAQPSKQC 236

RESULT 10
Q80XZ4 PRELIMINARY; PRT; 581 AA.
AC Q80XZ4;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-22 receptor alpha chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=22505377; PubMed=12618864;
RA Tachibiri A., Imamura R., Wang Y., Fukui M., Umamura M., Suda T.;
RT "Genomic structure and inducible expression of the IL-22 receptor
alpha chain in mice."
RL Genes Immun. 4:153-159(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Aiko T., Wang Y., Suda T.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY103454; AAM52222.1; -.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0004896; F: hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR008957; FN_III-like.
DR Receptor.
SQ SEQUENCE 581 AA; 63794 MW; A2BF8692BB8AA93B CRC64;

Query Match 21.2%; Score 263; DB 11; Length 581;
Best Local Similarity 33.0%; Pred. No. 2.6e-18;
Matches 63; Conservative 34; Mismatches 88; Indels 6; Gaps 4;

QY 31 QKVRFSQSRNFHNLHWQAGSSLPNNISYFVQYKMGQSQWEDKVDGCTGTTALFCDLTN 90
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DB 26 QHVKFSQSNFENILTWGGPA-STSDTVSYVEYKYGKRLAKAGCQRITQKFCNLIME 84
QY 91 TLDPELYYGRVMTACAGHSASWTRTPFTPMWETKLDPPVVTITRVNASLRVLLPPEL 150
DB 85 TRNHTFYAKVTAVSAGPPVTKMTDFPSLSQHTTIKPPDVTCIPKVSIOQLVHPTLT 144
QY 151 PNRNQGKNSM-ETYYGLVTRV-FTNNLSLEKQKAYEGTORAVEIEGLIPHSSYCVVA 208
DB 145 PVLSEGDGHQLTLEEIFHDLFVRLHLVHNTY---QMHLEKQREYFGLTPTDFEFLGSI 201
QY 209 ENYQPMFDRS 219
DB 202 TITFILSKES 212

RESULT 11
Q8N6P7 PRELIMINARY; PRT; 574 AA.
AC Q8N6P7;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin 22 receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal cortex;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BCC29273; AAH29273.1; -.
DR Genew; HGNC:13700; IL22RA1.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0004896; F: hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR008957; FN_III-like.
DR Receptor.
SQ SEQUENCE 574 AA; 63076 MW; D46CCT71D496F3420 CRC64;

Query Match 20.5%; Score 254; DB 4; Length 574;
Best Local Similarity 32.5%; Pred. No. 2.2e-17;
Matches 69; Conservative 31; Mismatches 106; Indels 6; Gaps 4;

QY 10 LLIILLSSATEIQPARVSLTPKVRFSQSRNFHNLHWQAGSSLPNNISYFVQYKMGQSQ 69
DB 5 LTLITVGSLLAAHAPDPSDLLQHVFSQSNFENILTWDSGPB-GTPDVYSIEYKTYGR 63
QY 70 QWEDKVDGCTGTTALFCDLTNETLDPYELYYGRVMTACAGHSASWTRTPFTPMWETKLDP 129
DB 64 DWVAKGQCRITRKSCNLTAVETGNLTLYYARVAVSAGRSATKMTORFSSLOHTTLKP 123
QY 130 PVVTITRVNASLRVLLPPELNRNQGKNSM-ETYYGLVTRV-FTNNLSLEKQKAYE 187
DB 124 PDVTCISKVRSIQMIVHPPTPTIRAGDGHRLTDEIDFHLFVHLELVNRY---QMHLG 180
QY 188 GTORAVEIEGLIPHSSYCVVAENYQPMFDRS 219
DB 181 GKQREYFGLTPTDFEFLGIMICVPTWAKES 212

RESULT 12
Q9HB22 PRELIMINARY; PRT; 574 AA.
AC Q9HB22;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE IL-22 receptor.
GN IL22R.
```

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20469498; PubMed=10875937;  
RA Xie M.H., Aggarwal S., Ho W.H., Foster J., Zhang Z., Stinson J.,  
RA Wood W.I., Goddard A.D., Gurney A.B.;  
RT "Interleukin (IL)-22, a Novel Human Cytokine That Signals through the  
RT Interferon Receptor-related Proteins CRF2-4 and IL-22R.";  
RL J. Biol. Chem. 275:31335-31339(2000).  
DR EMBL: AF286095; AAG22073.1; --  
DR HSSP: P133726; 1TEH  
DR GO: GO:0016020; C:membrane; NAS  
DR GO: GO:0004904; F:interferon receptor activity; TAS.  
DR DR InterPro; IPR000282; Cytok\_receptor\_2.  
DR InterPro; IPR008957; FN\_III-like.  
KW Receptor.  
SQ SEQUENCE 574 AA; 62977 MW; C179C7085C6F3420 CRC64;  
  
Query Match 20.5%; Score 254; DB 4; Length 574;  
Best Local Similarity 32.5%; Pred. No. 2.2e-17;  
Matches 69; Conservative 31; Mismatches 106; Indels 6; Gaps 4;  
  
QY 10 LLILASSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPNNNSIYFVQYKYGOS 69  
DB 5 LTILVGLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGE-GTPTDVTYSIEYKTYGER 63  
  
QY 70 QWEDKVCWGTTFALFCDLTNETLDPVLYGYRYWTACAGHSAWTPRFTPWETKLPD 129  
DB 64 DWAKGCGQIRTKSCNLTVEGLNLTETLYIYRTAVSAGRSATKMTDFSSLOHTLKP 123  
  
QY 130 PVVTITRVNASLRVLLRPPPELRNOSGKNASME-TYIGLVYRV-FTINNSLEKEQAYE 187  
DB 124 PDVTCISKVRSIQMVHPTPTPIRAGDGHRLTLEDIFDLYHLEQVARTY---QMHLG 180  
  
QY 188 GTQRAVEIEGLPHSSYCVVAEYQPFDRRS 219  
DB 181 GKQREYEFFGLTPTDTEFLGTLMICVPTWAKES 212  
  
RESULT 13  
Q96SH7 PRELIMINARY; PRT; 209 AA.  
ID Q96SH7  
AC Q96SH7  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE BA204P2.1.3 (Interleukin 20 receptor alpha, isoform 3).  
GN IL20RA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Griffiths C.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL135902; CAC38376.1; --  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
DR InterPro; IPR008957; FN\_III-like.  
KW Receptor.  
SQ SEQUENCE 209 AA; 23616 MW; 467AB77BE3840361 CRC64;  
  
Query Match 19.1%; Score 237.5; DB 4; Length 209;  
Best Local Similarity 31.8%; Pred. No. 3e-16;  
Matches 57; Conservative 22; Mismatches 87; Indels 13; Gaps 3;  
  
QY 30 PQKVFQSRNFHNLHWQAGSSLPNNNSIYFVQYKYGOSQWEDKVCWGTTFALFCDLTN 89

DB 40 PANITFSLNKNVQLQWTPPEGLQGVKVTYVQYFIYQKQKMLNKSECRNINRTYCDLSA 99  
QY 90 ETLDPELYYGRVWTACAGHSAWTPRFTPWETKLPDPPVVTITRVNASLRVLLRPPPE 149  
DB 100 ETSDEYHQYAKVKAIWGTRKCSKWAESGRFYPLETQIGPFEVALTTDEKSIISVLTAE 159  
QY 150 LPNRNOSGKNASMETTY-GLVYRVFTINNSLEKEQAYEGTQRAVEIE-GLIPHSSY 205  
DB 160 KWKENPEDLPVSNQOIYVNLKYNVSLNTR-----SNRTVSLKWNAGYIHVPLC 208  
  
RESULT 14  
Q7ZT05 PRELIMINARY; PRT; 203 AA.  
ID Q7ZT05  
AC Q7ZT05;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Helical cytokine receptor CRFB9.  
GN CRFB9.  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lutfalla G., Roest Crolius H., Stange-Thomann N., Jaillon O.,  
RA Mogensen K., Monneron D.;  
RT "Comparative genomic analysis reveals independent expansion of a  
RT lineage-specific gene family in vertebrates: The class II cytokine  
RT receptors and their ligands in mammals and fish";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Lutfalla G.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ544912; CAD67770.1; --  
DR EMBL: AJ544895; CAD67783.1; --  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
KW Receptor.  
SQ SEQUENCE 203 AA; 22779 MW; 9F1E843FA4E75E82 CRC64;  
  
Query Match 17.3%; Score 215; DB 13; Length 203;  
Best Local Similarity 29.3%; Pred. No. 6.2e-14;  
Matches 65; Conservative 33; Mismatches 90; Indels 34; Gaps 7;  
  
QY 8 LGLLIILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPNNNS--IYFVQYK 65  
DB 11 LGTLGTLCGAVQDLAP-----PTNLAFDSVDYKNVLSW-----SPPANGSSLLYDVQWKI 60  
  
QY 66 YGQSQWEDKVCWGTTFALFCDLTNETLDPVLYYGRVWTACAGHSAWTPRFTPWET 125  
DB 61 YGDPDWLDAASCRTQKLCRLDSSETSVPREYIYARVPVITA-----PHTP-----AA 108  
  
QY 126 KLDPPVVTITRVNASLRVLLRPPPELRNOSGKNASMETTYGLVYRVFTINNSLEKEQKA 185  
DB 109 RISPPVLKIKVQKVVQVVEPPLHIR-----KMHSSLOPKIYLTHPSGEEELFL 159  
QY 186 YEGTQRAVEIEGLIPHSSYCVVAEYQPFDRRSRPRKXERC 227  
DB 160 VDPRSRKLTLH-LRHQRVCVQAQTQILLQAKSSARSPTTCV 200  
  
RESULT 15  
Q800G1 PRELIMINARY; PRT; 568 AA.  
ID Q800G1  
AC Q800G1;

Search completed: March 12, 2004, 15:59:34  
Job time : 46 secs